

Kelp forest eco-evolutionary dynamics

J. David Aguirre, Vanessa Arranz,
Jose I. Carvajal and Libby Liggins

J.D.Aguirre@massey.ac.nz

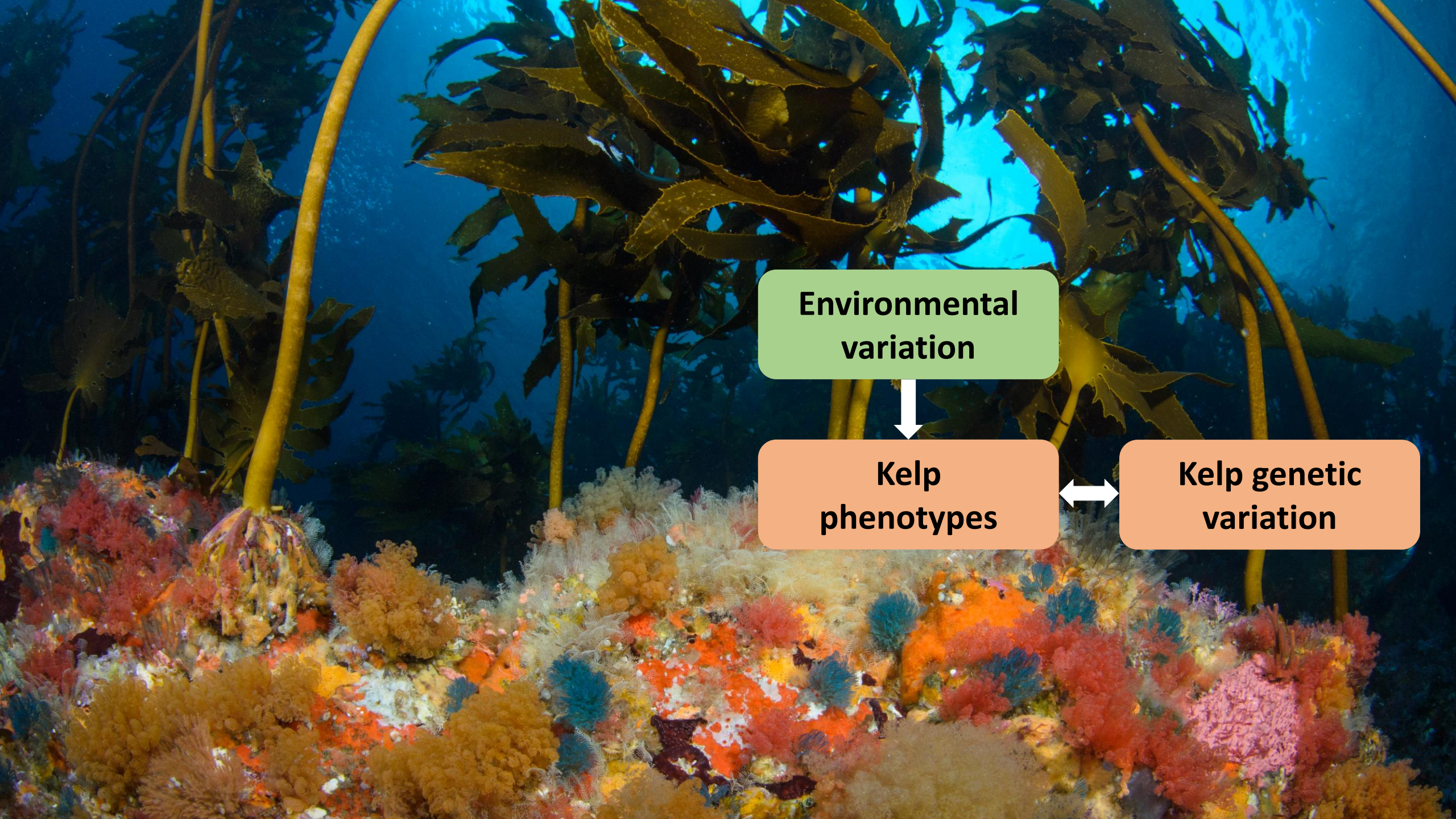




Photo: seacologynz.com



**Kelp
phenotypes**



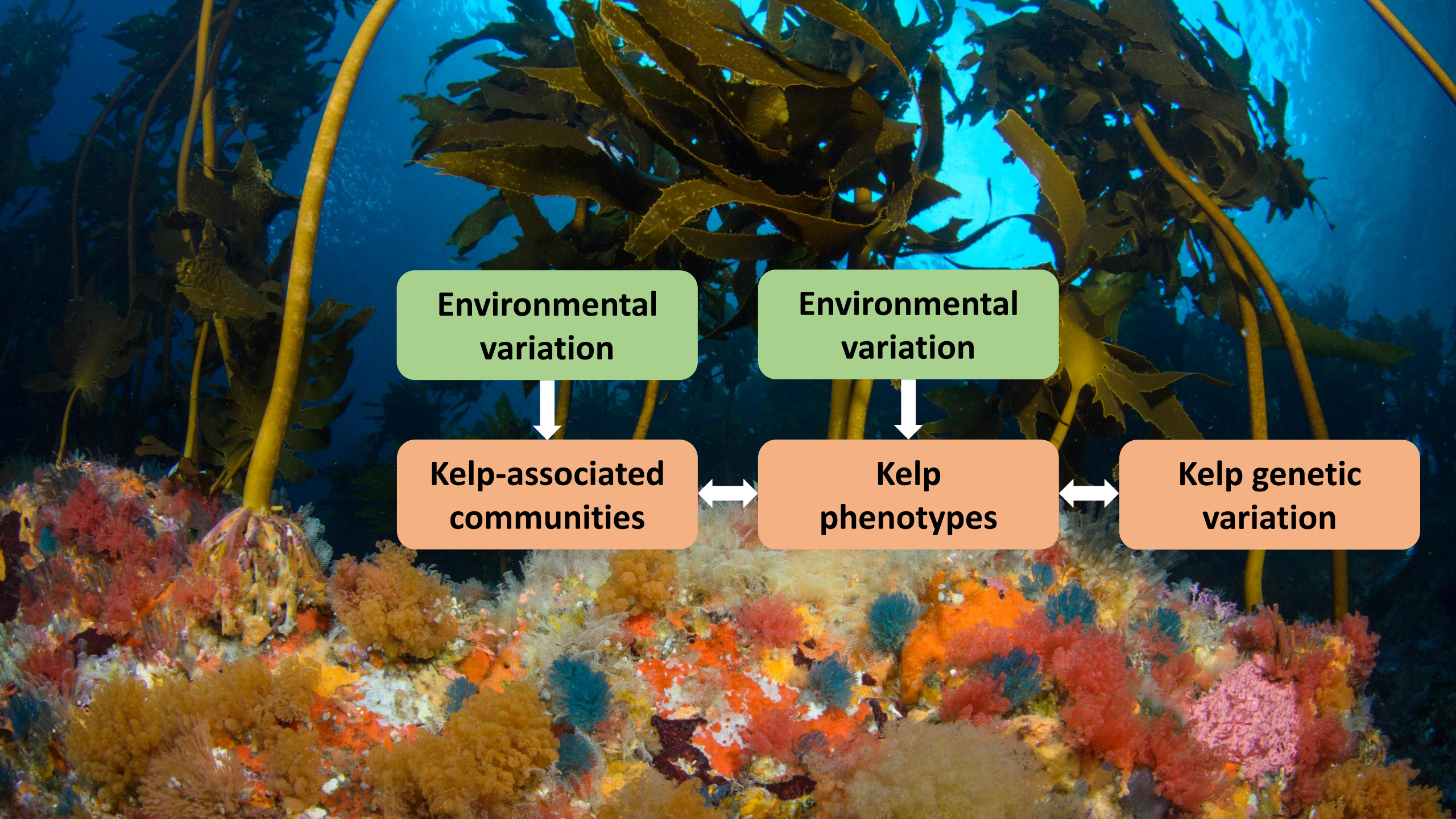
**Environmental
variation**



**Kelp
phenotypes**



**Kelp genetic
variation**



**Environmental
variation**

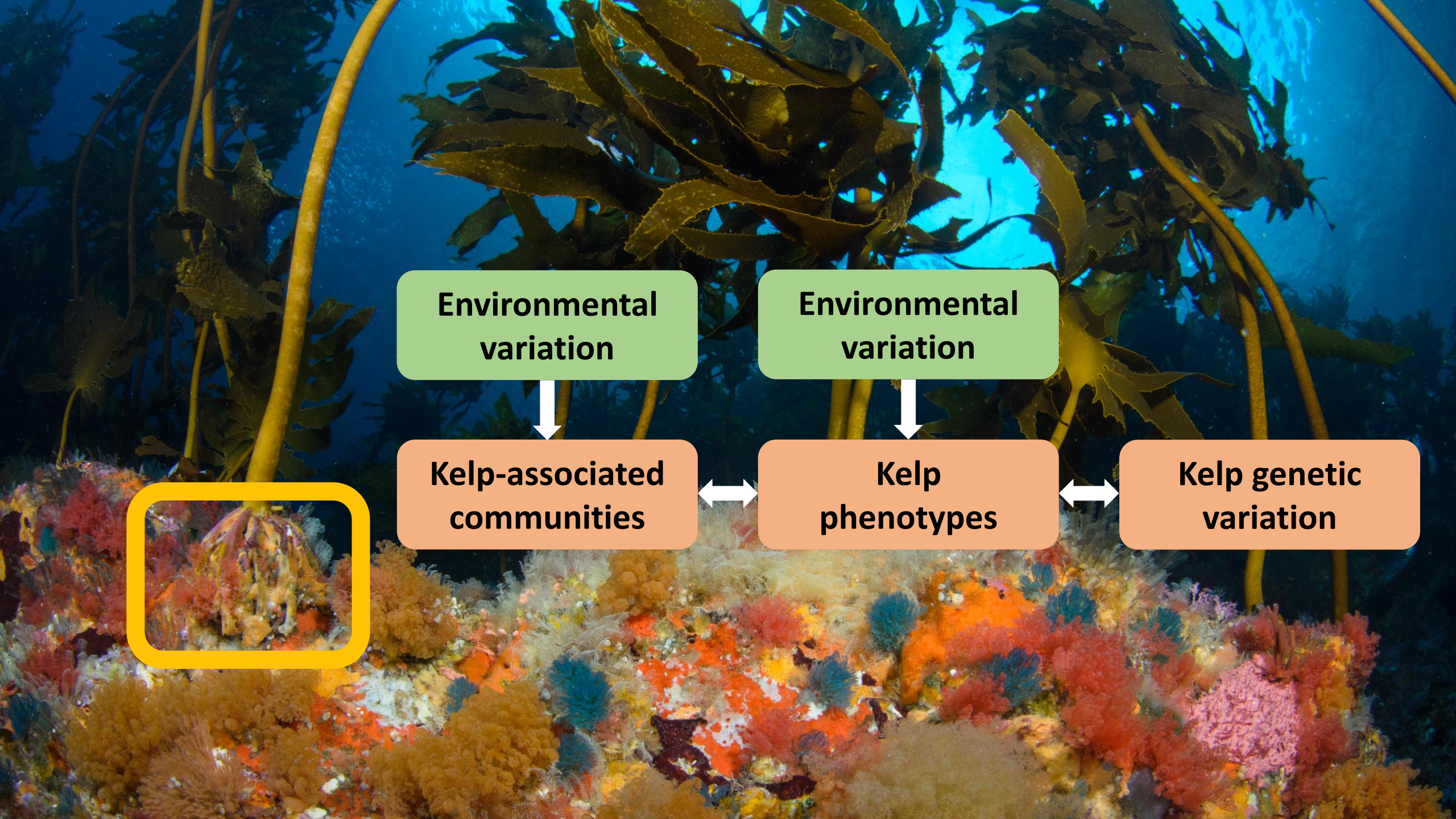
**Environmental
variation**

**Kelp-associated
communities**

**Kelp
phenotypes**

**Kelp genetic
variation**





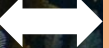
**Environmental
variation**

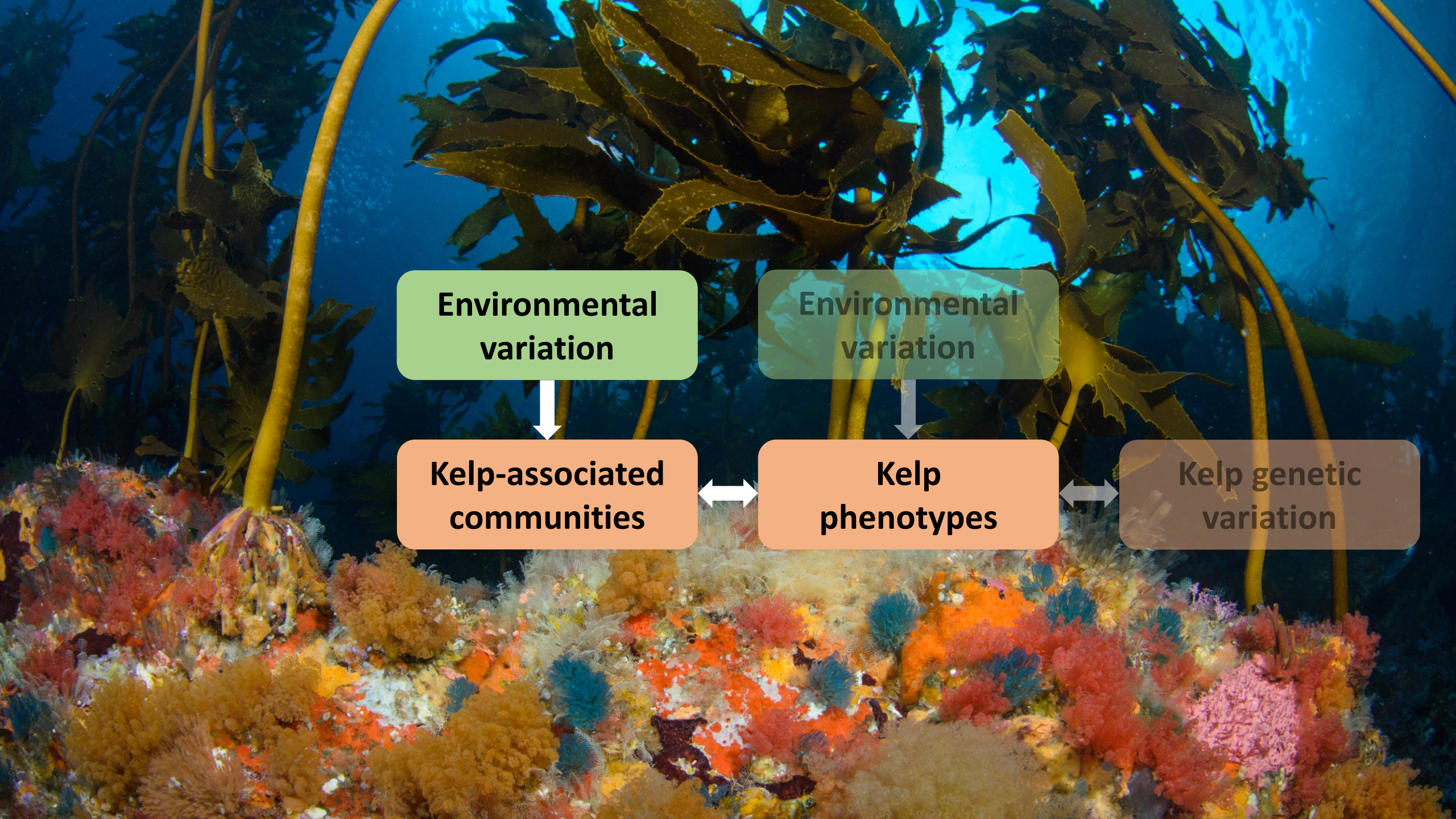
**Environmental
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**Kelp genetic
variation**





**Environmental
variation**

**Environmental
variation**

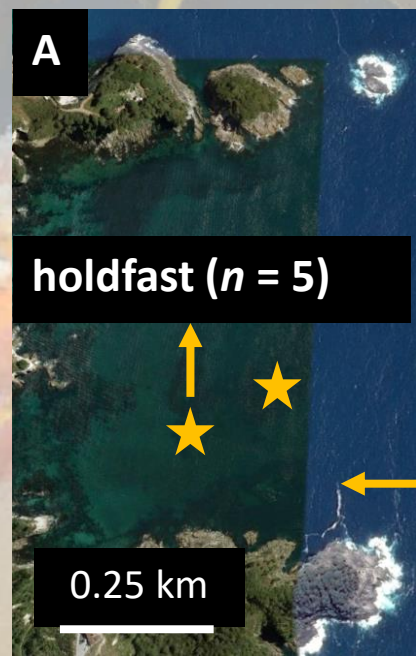
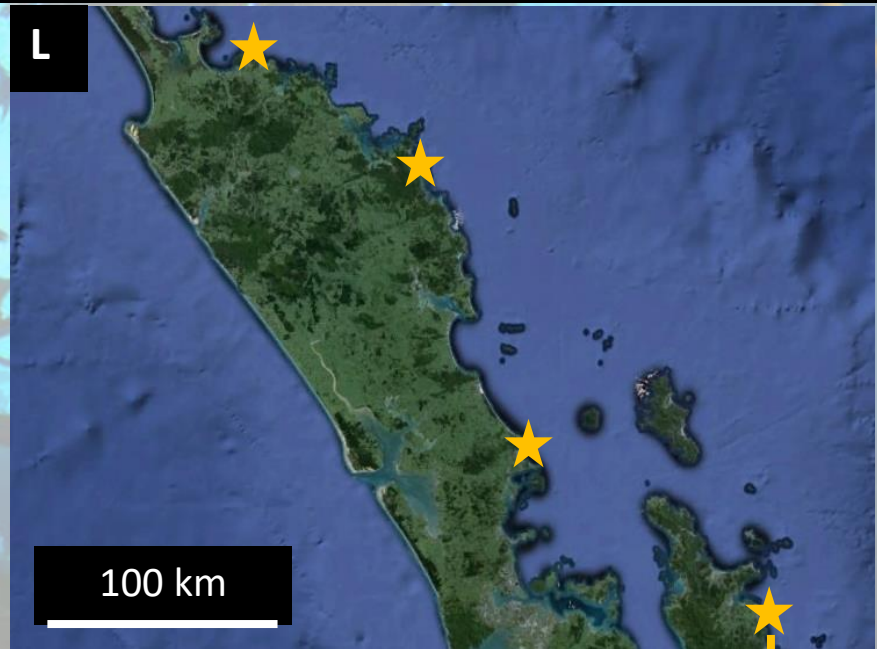
**Kelp-associated
communities**

**Kelp
phenotypes**

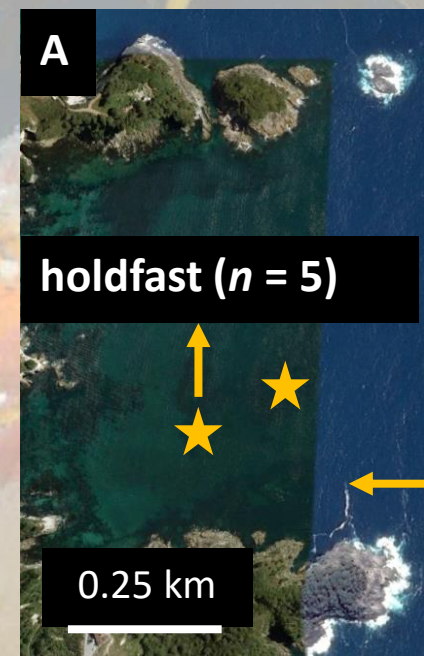
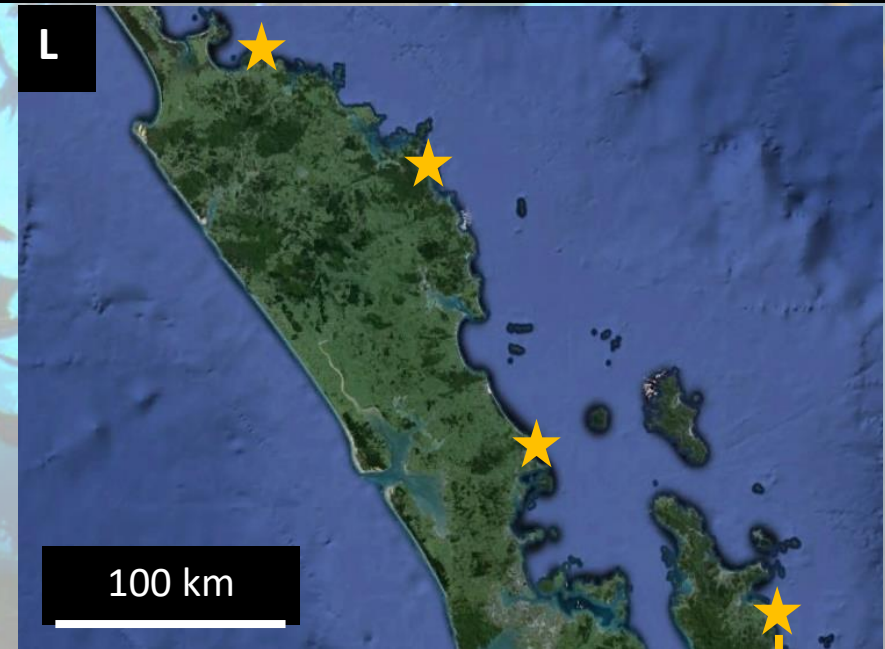
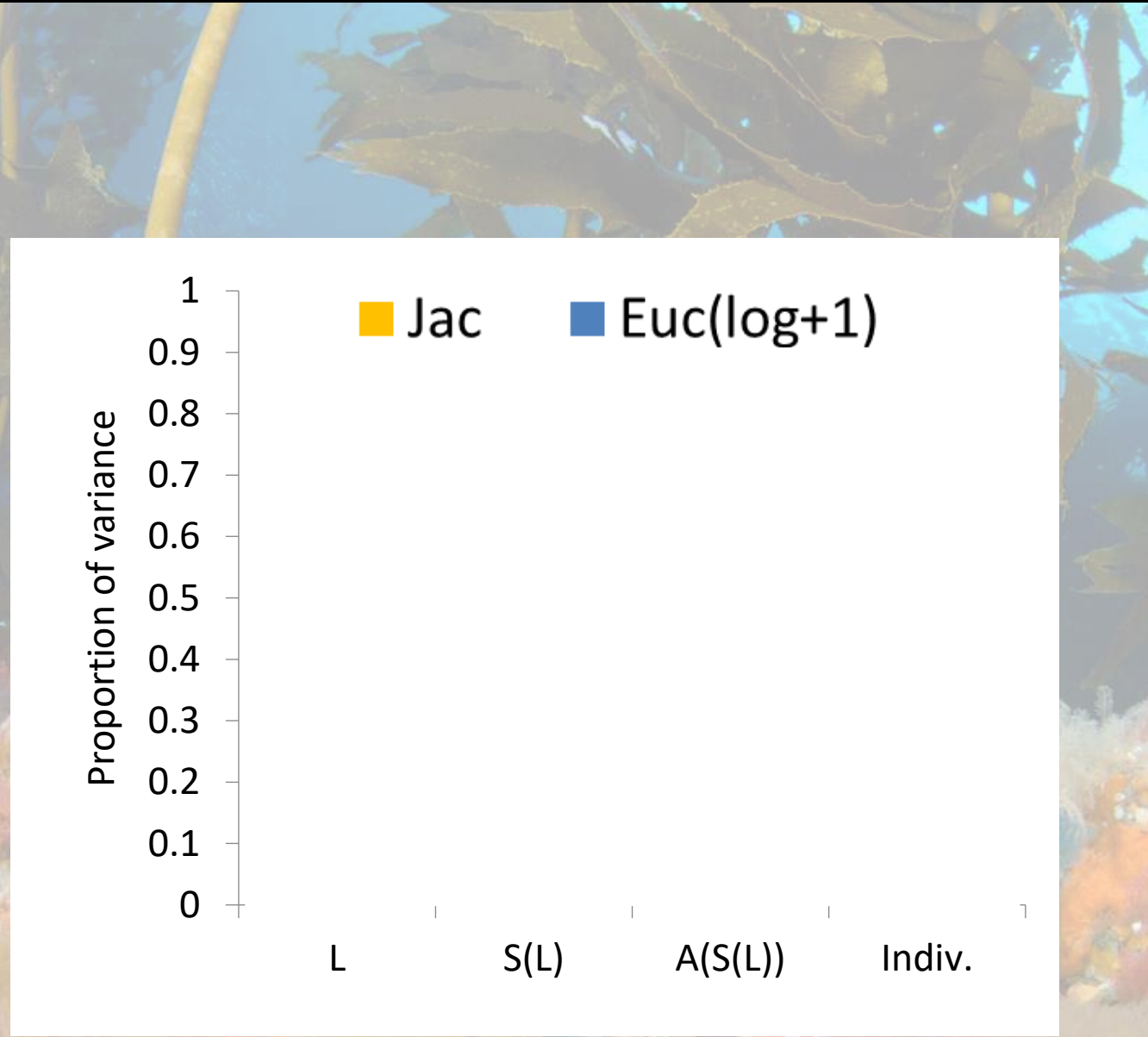
**Kelp genetic
variation**



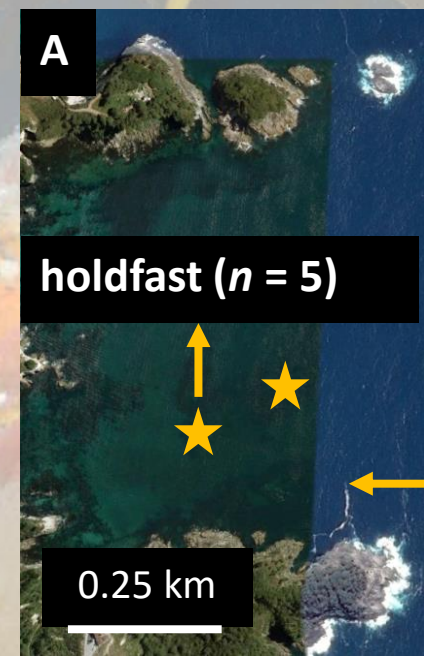
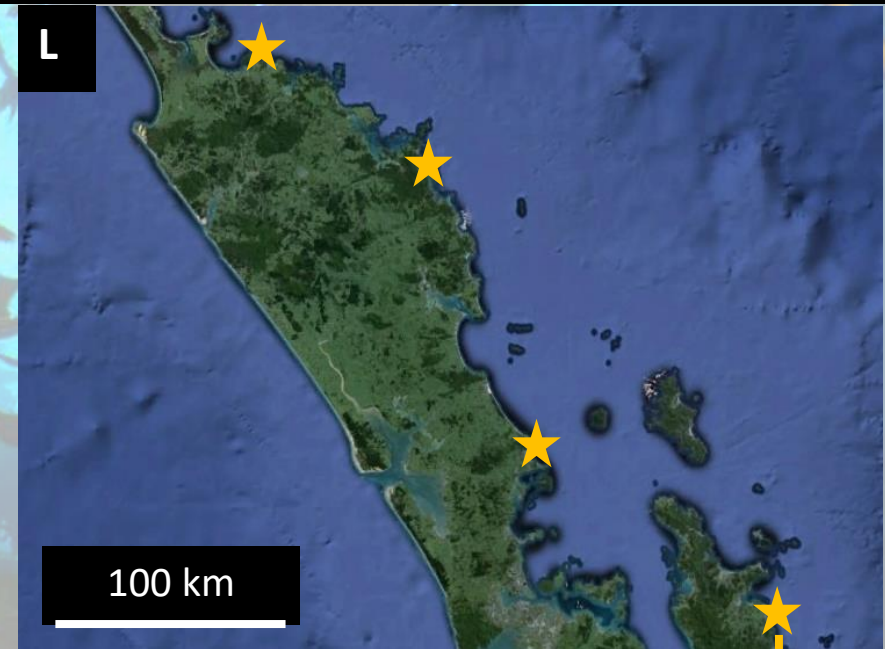
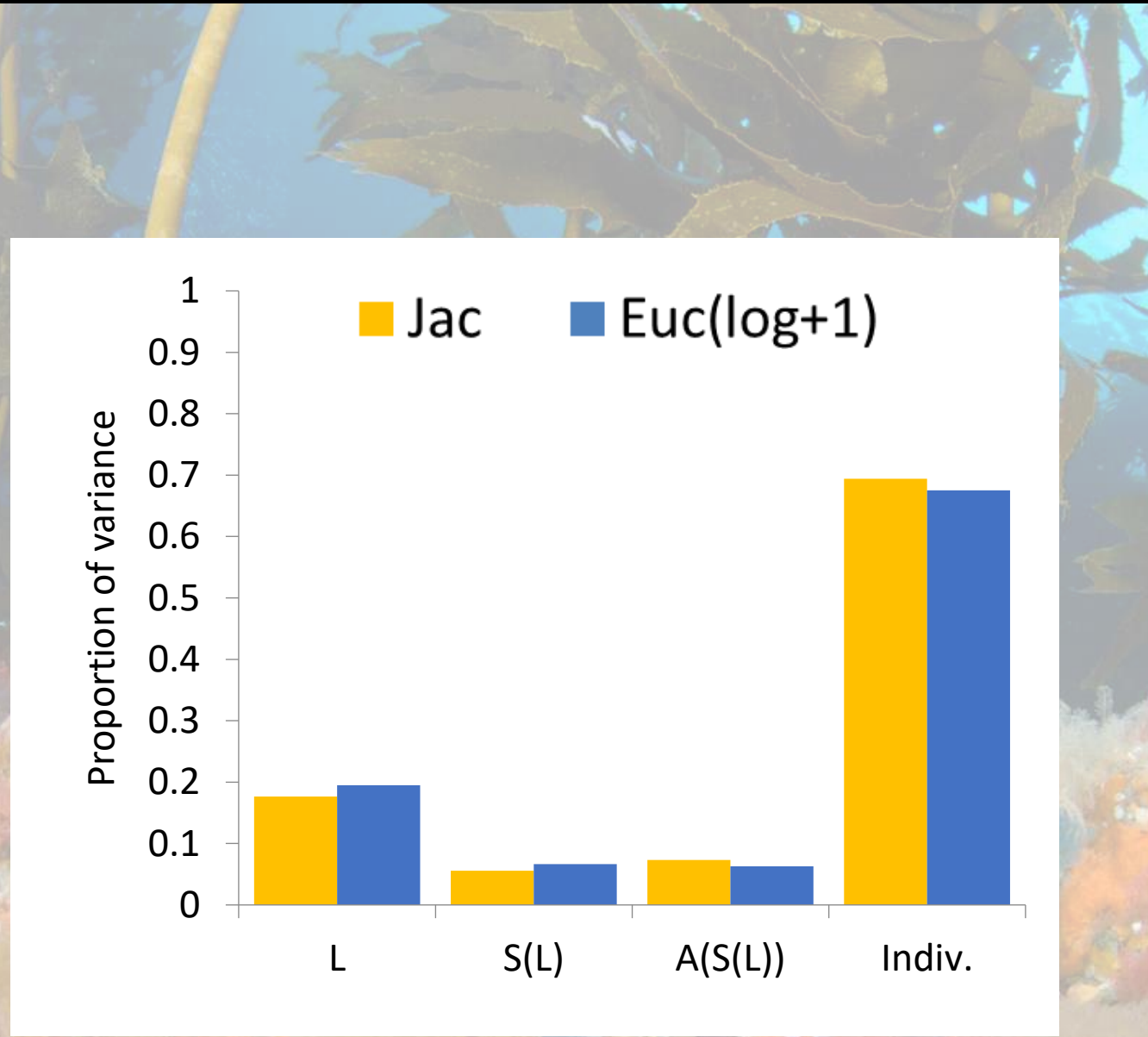
Partitioning biogeographic variation in holdfast community composition

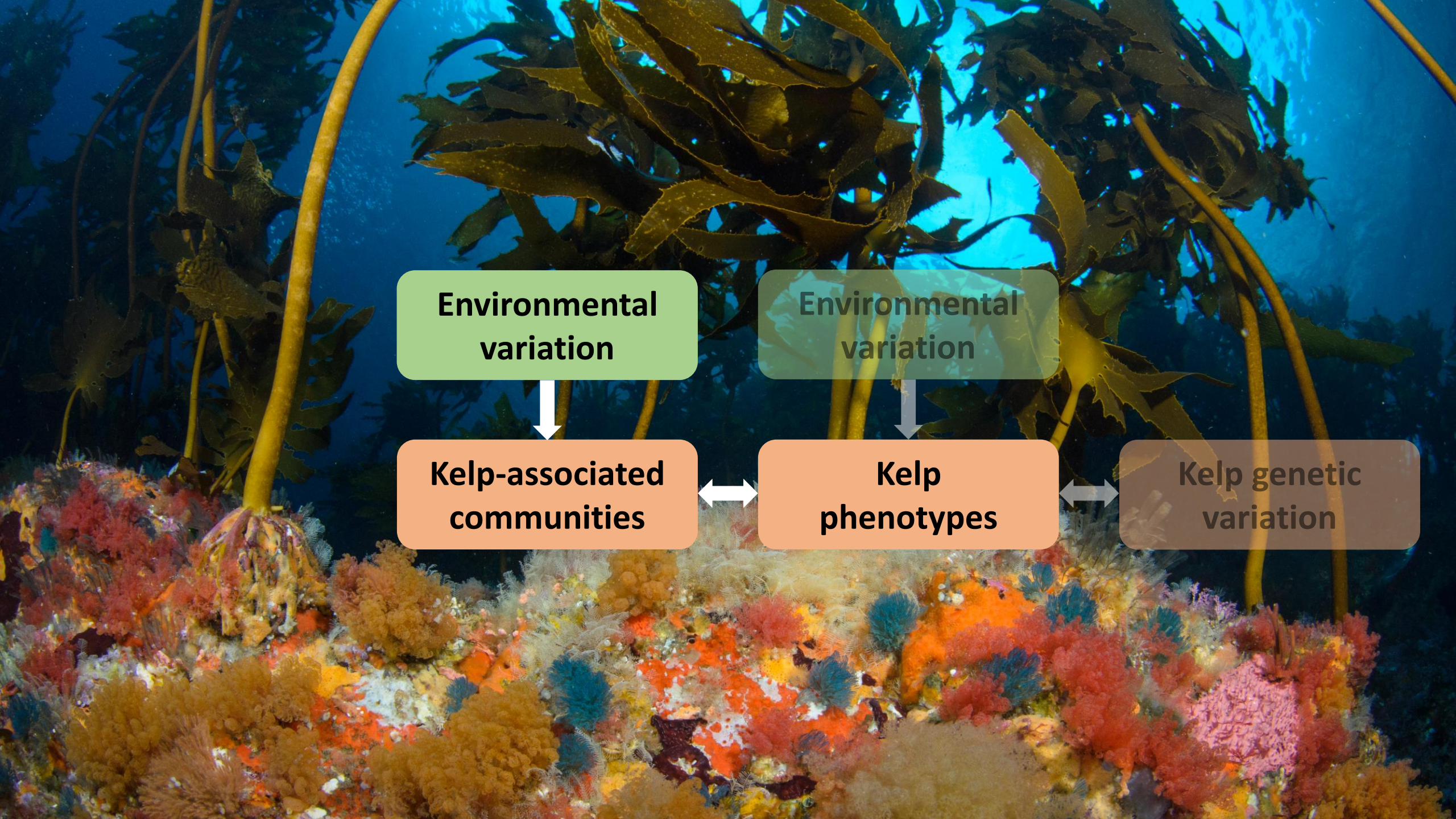


Partitioning biogeographic variation in holdfast community composition



Variability in community composition strongly influenced by holdfast ID





**Environmental
variation**

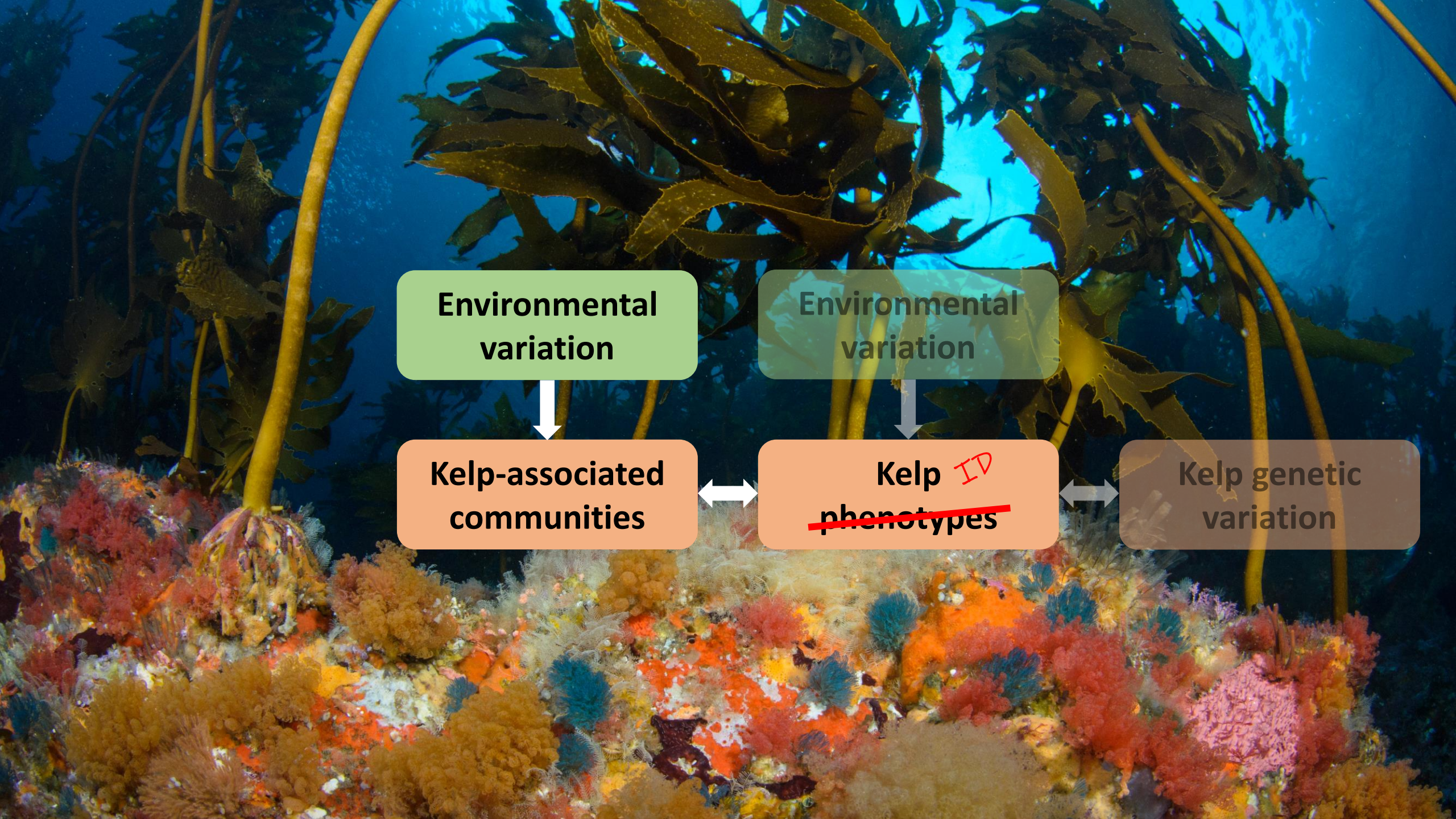
**Environmental
variation**

**Kelp-associated
communities**

**Kelp
phenotypes**

**Kelp genetic
variation**





Environmental
variation

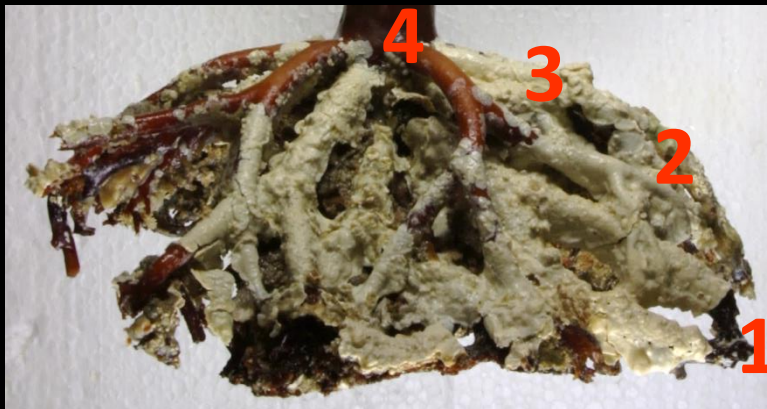
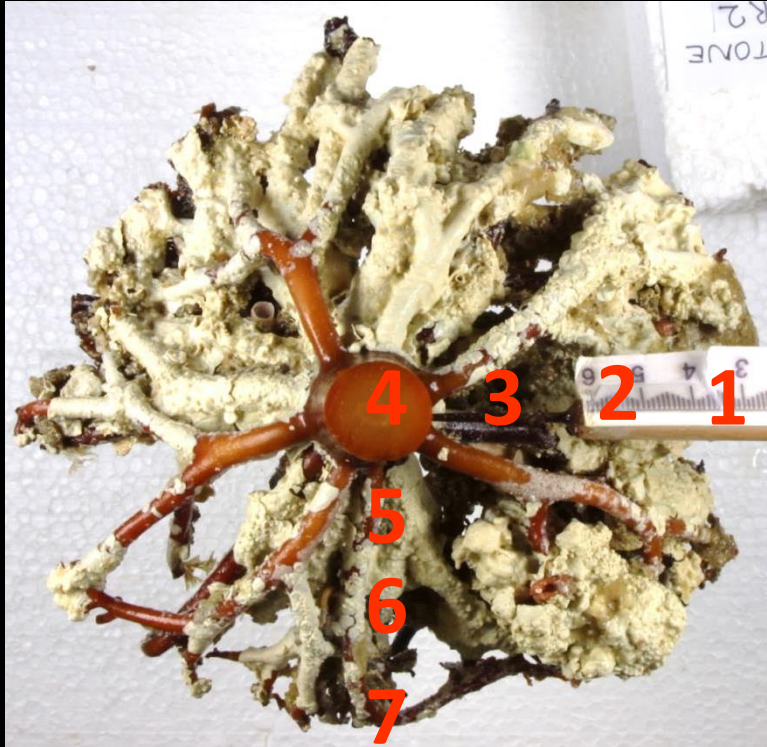
Environmental
variation

Kelp-associated
communities

Kelp ~~phenotypes~~ ID

Kelp genetic
variation

Describing holdfast phenotypes - Geometric morphometrics



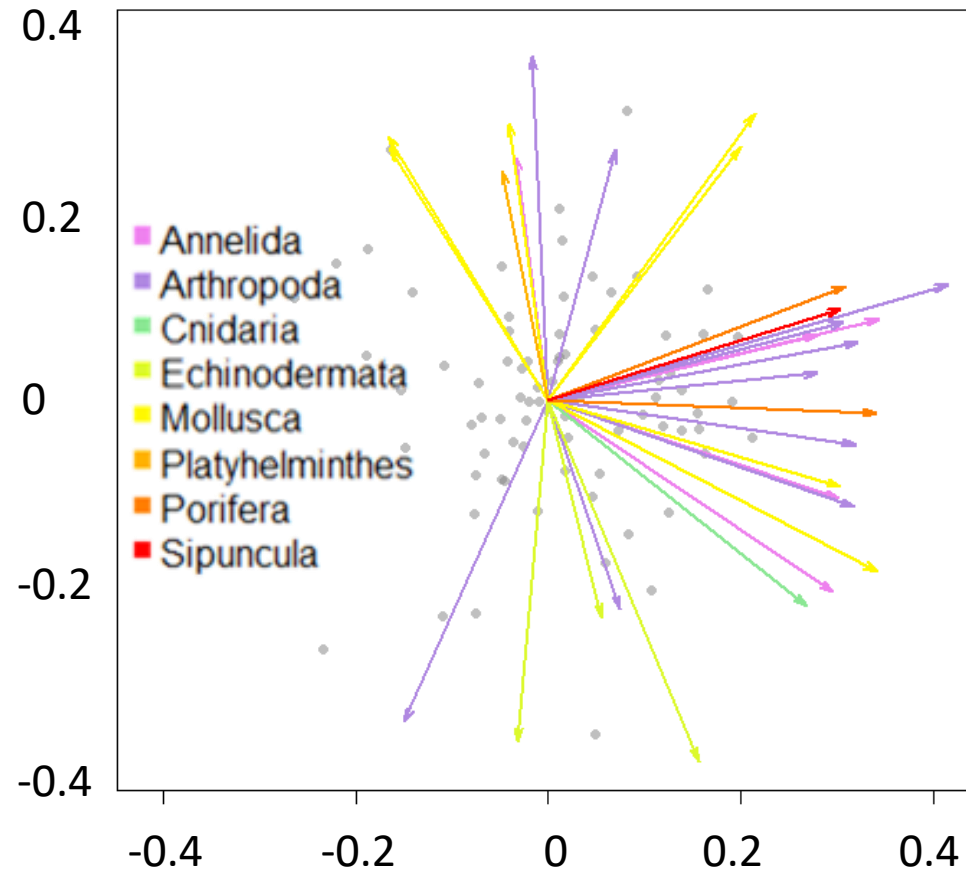
[X, Y, Z] coordinates for 7 landmarks
spanning two radial axes

Steiner Symmetrisation

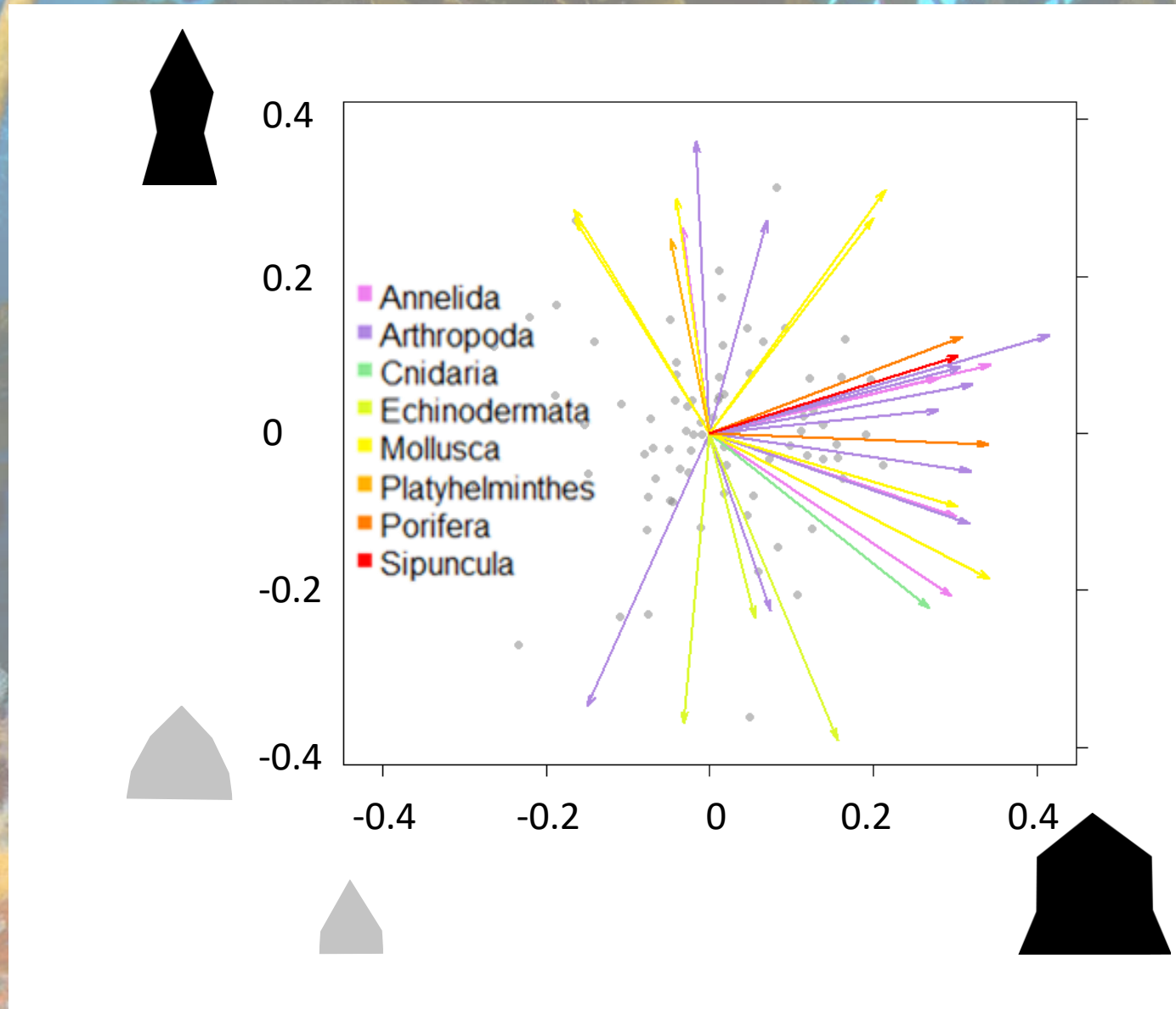
Generalized procrustes rotation¹

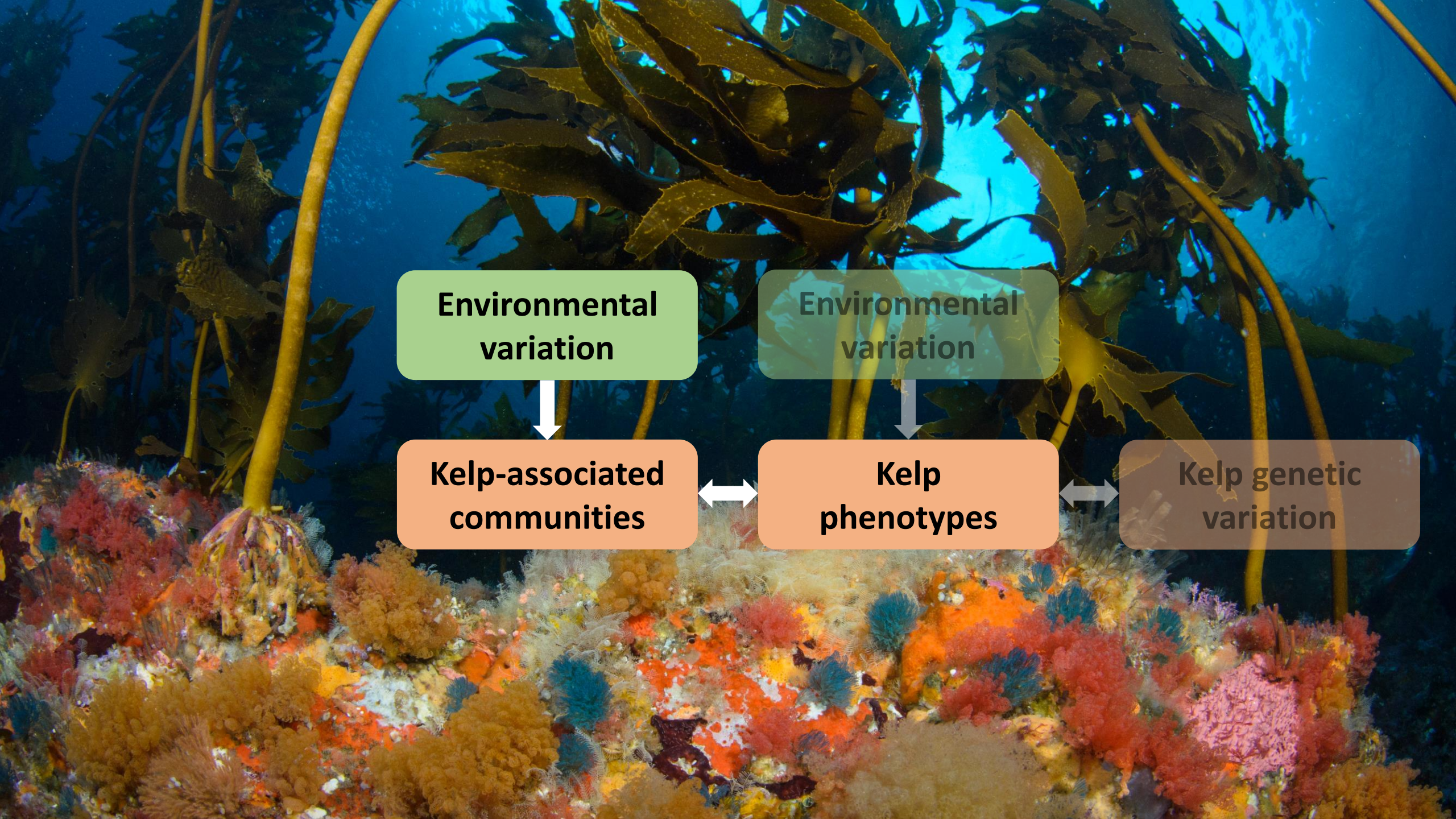
¹Geomorph R package

Distinct phyla respond to differences in holdfast phenotypes



Distinct phyla respond to differences in holdfast phenotypes





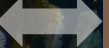
**Environmental
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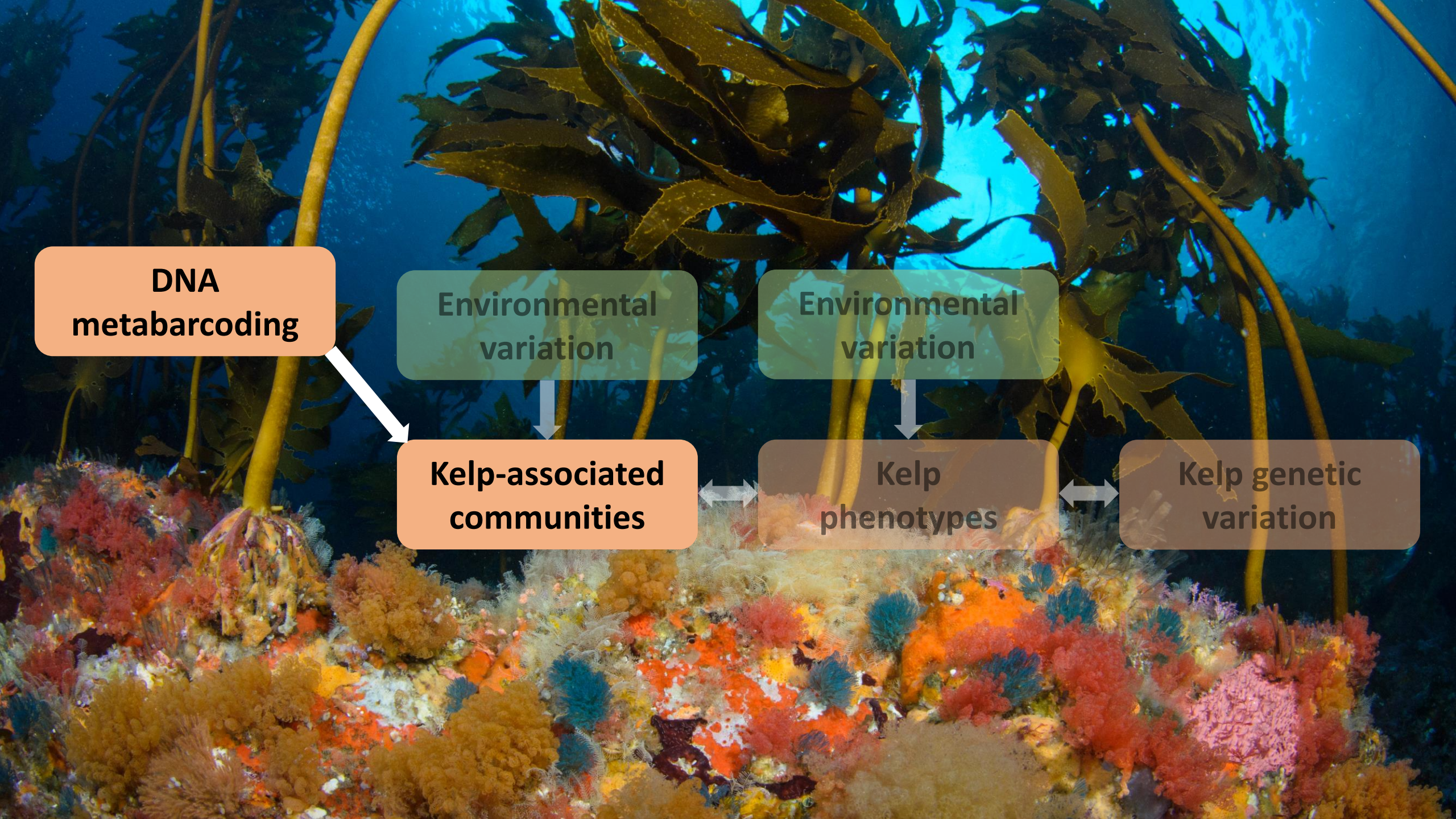
**Environmental
variation**

**Kelp-associated
communities**

**Kelp
phenotypes**

**Kelp genetic
variation**





**DNA
metabarcoding**

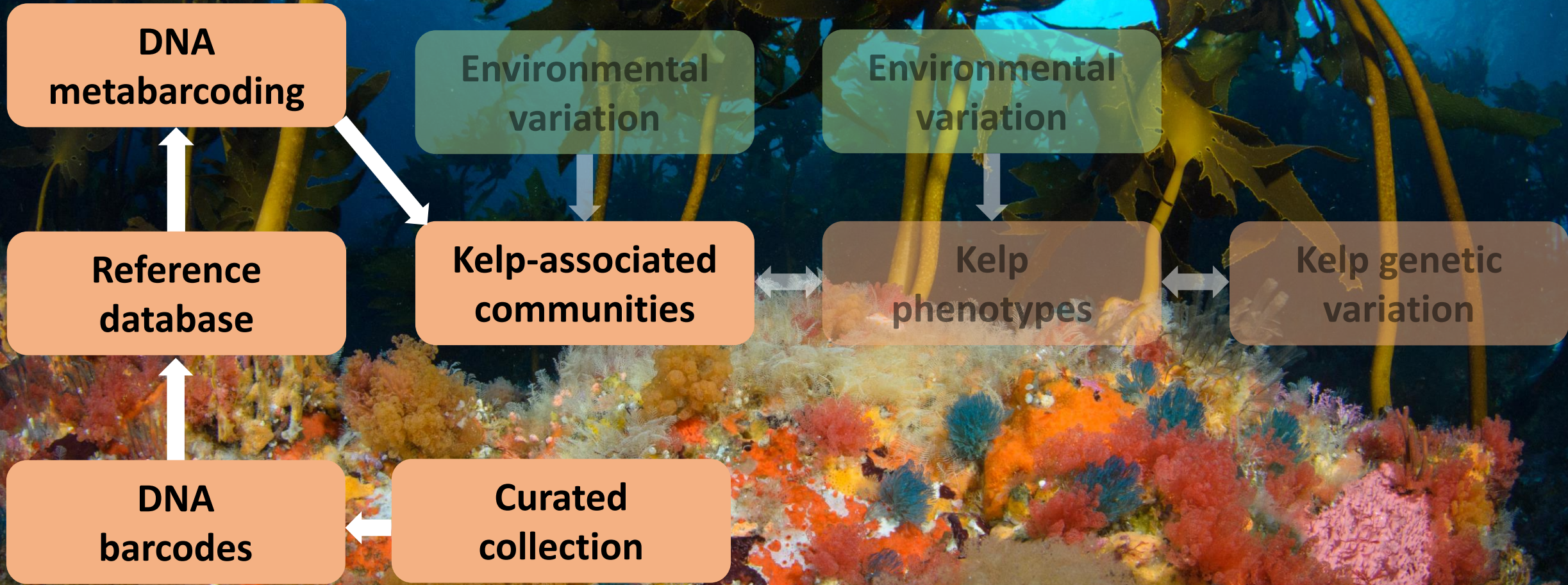
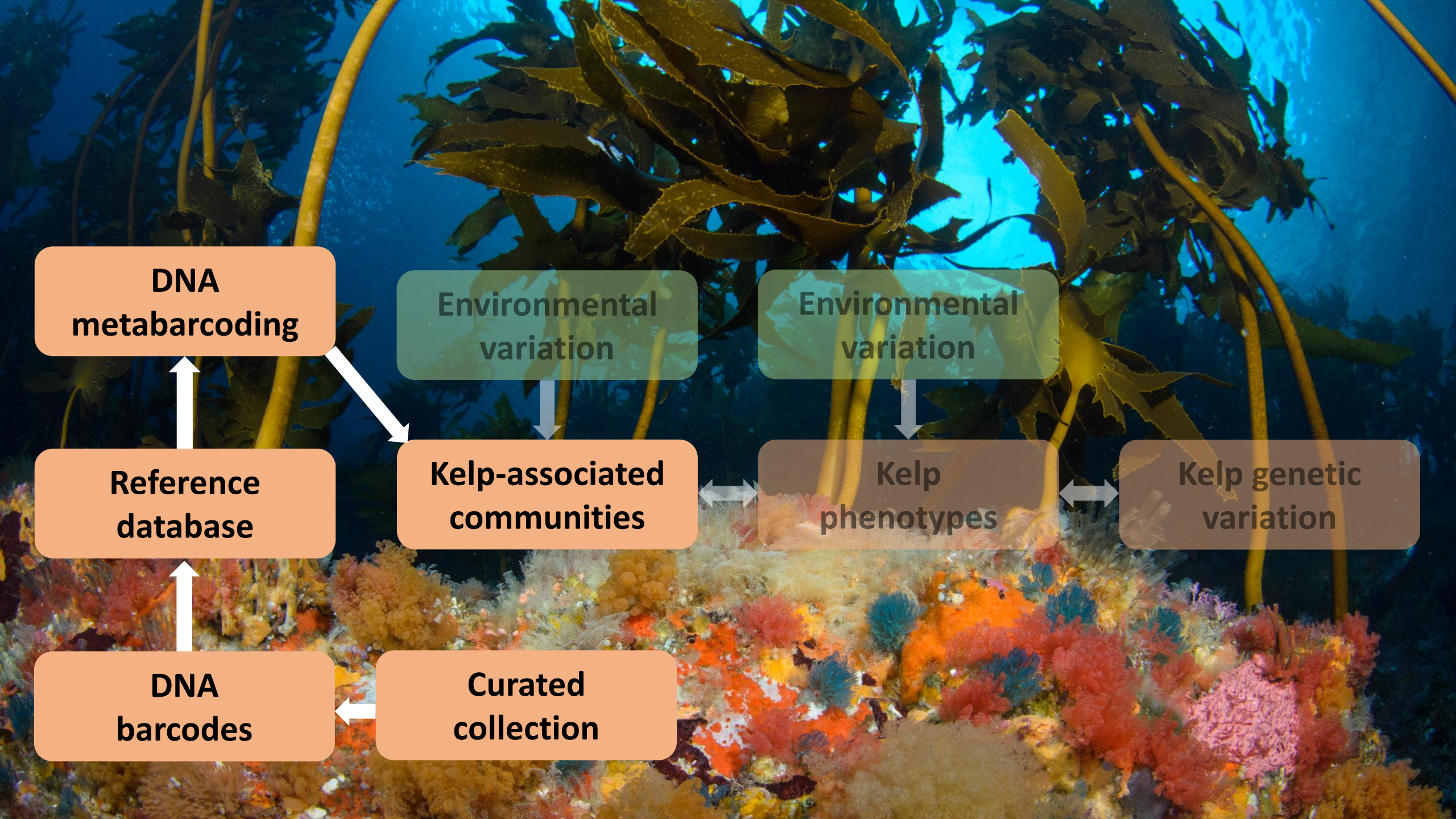
**Environmental
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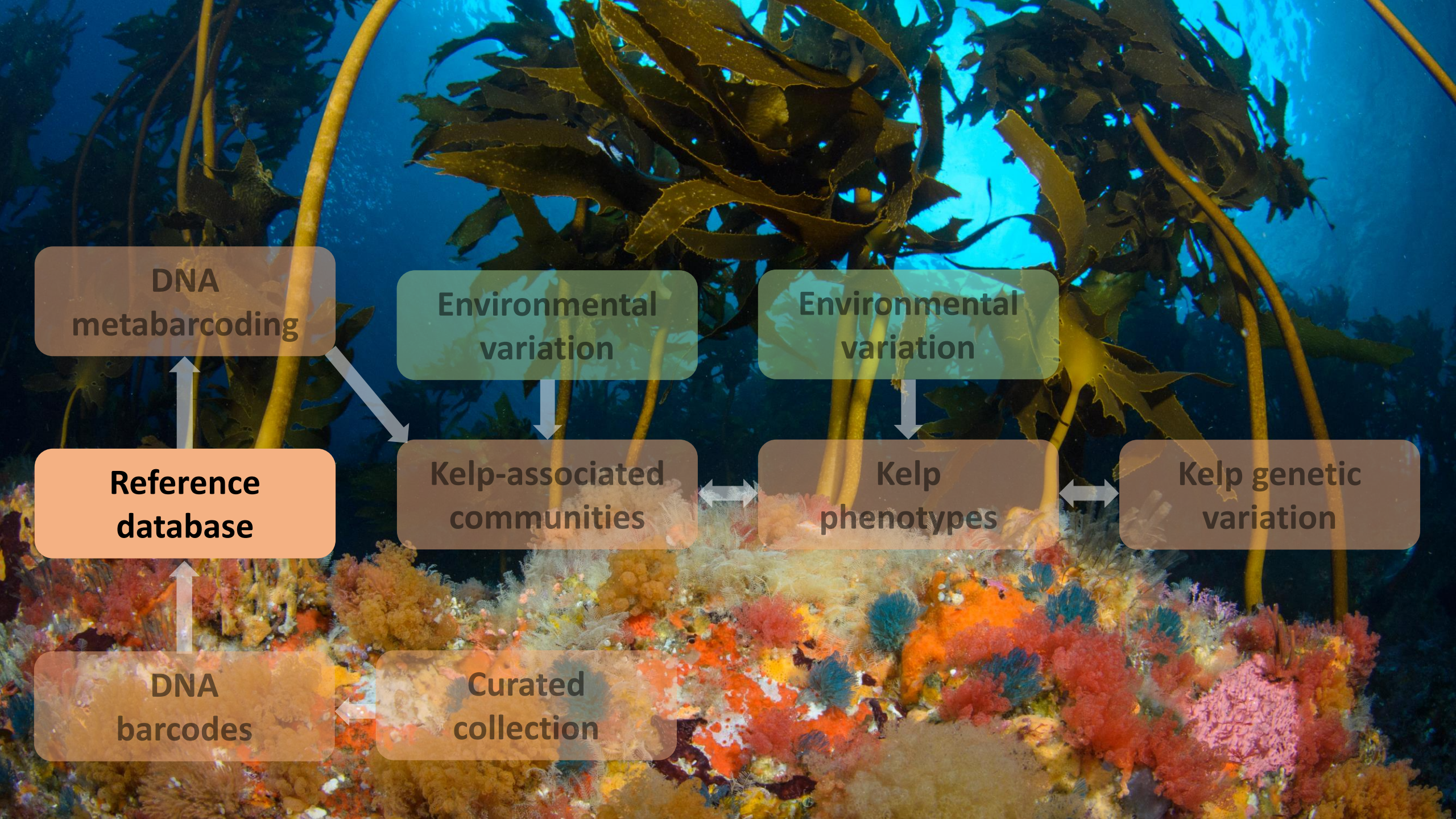
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**Kelp
phenotypes**

**Kelp genetic
variation**





DNA
metabarcoding

Environmental
variation

Environmental
variation

Reference
database

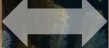
Kelp-associated
communities

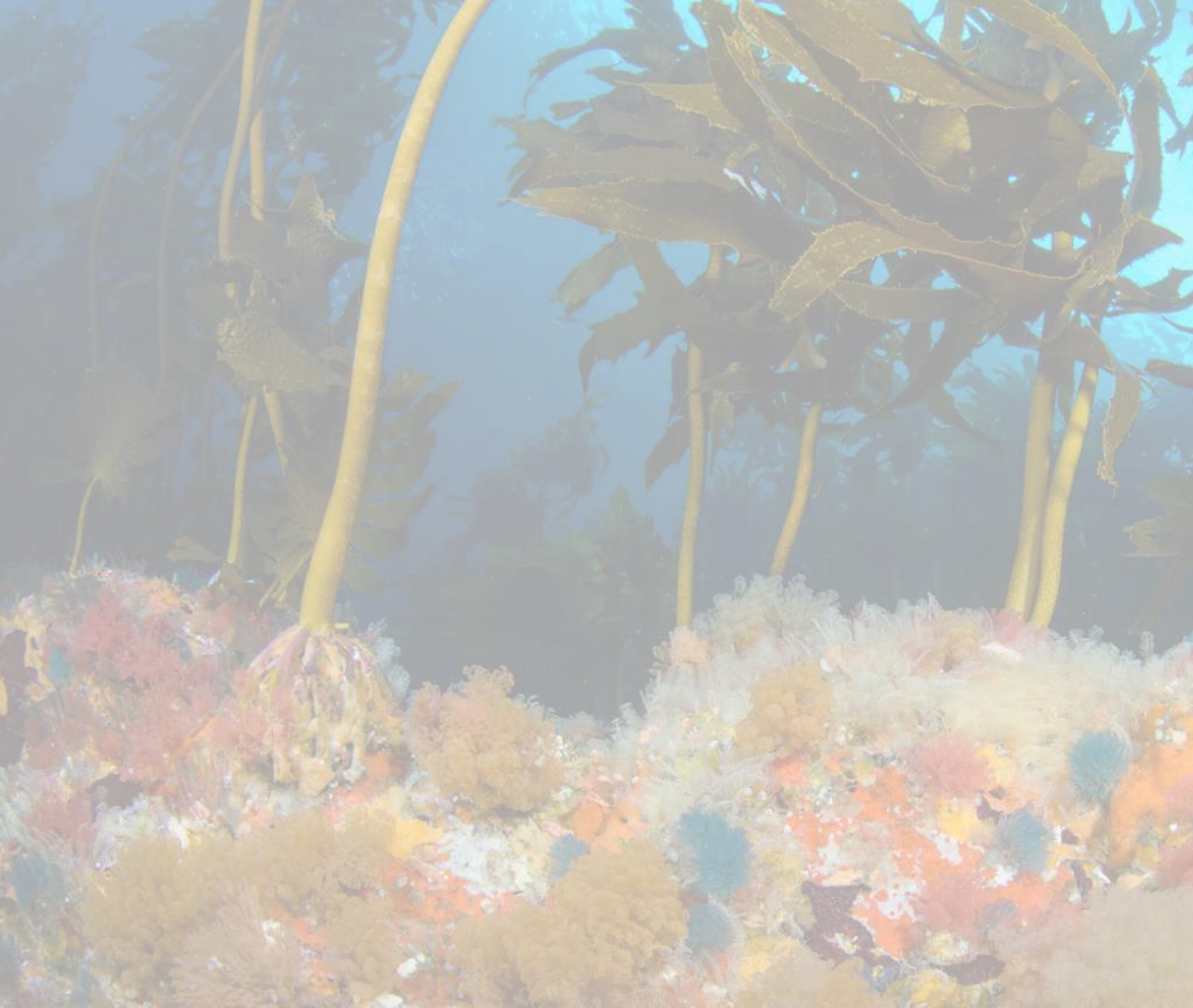
Kelp
phenotypes

Kelp genetic
variation

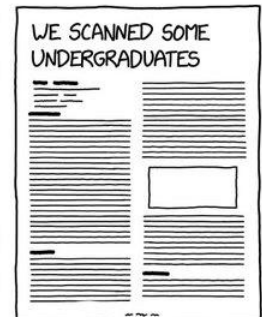
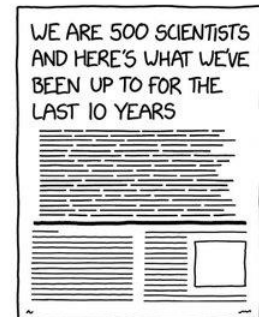
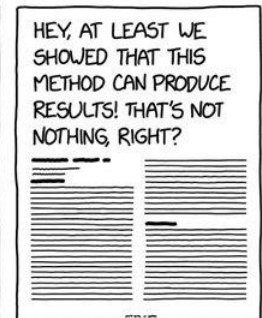
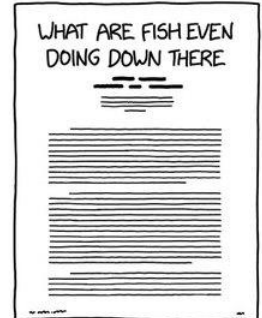
DNA
barcodes

Curated
collection





TYPES OF SCIENTIFIC PAPER



Data Descriptor | [Open Access](#) | Published: 03 July 2020

MARES, a replicable pipeline and curated reference database for marine eukaryote metabarcoding

Vanessa Arranz , William S. Pearman, J. David Aguirre & Libby Liggins

Scientific Data **7**, Article number: 209 (2020) | [Cite this article](#)

2283 Accesses | **1** Citations | **23** Altmetric | [Metrics](#)



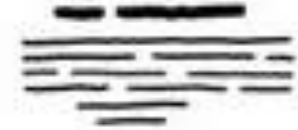
TYPES OF SCIENTIFIC PAPER

WE PUT A CAMERA
SOMEWHERE NEW

HEY, I FOUND A TROVE
OF OLD RECORDS! THEY
DON'T TURN OUT TO BE

MY COLLEAGUE IS
WRONG AND I CAN
FINALLY PROVE IT

THIS TASK I HAD TO DO
ANYWAY TURNED OUT
TO BE HARD ENOUGH
FOR ITS OWN PAPER



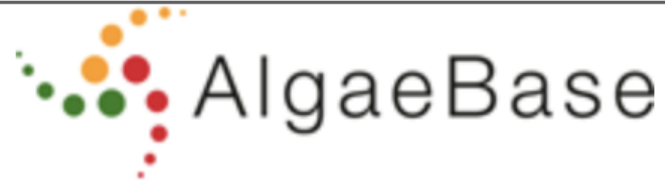
~ ~ ~



MARES – Reference sequence database



BOLD
SYSTEMS



OSFHOME ▾

MARES Custom Metabarcoding Database

Files

Wiki

Analytics

Registrations

MARES Custom Metabarcoding Database

Contributors: [Vanessa Arranz](#), [William Pearman](#), [J David Aguirre](#), [Libby Liggins](#)

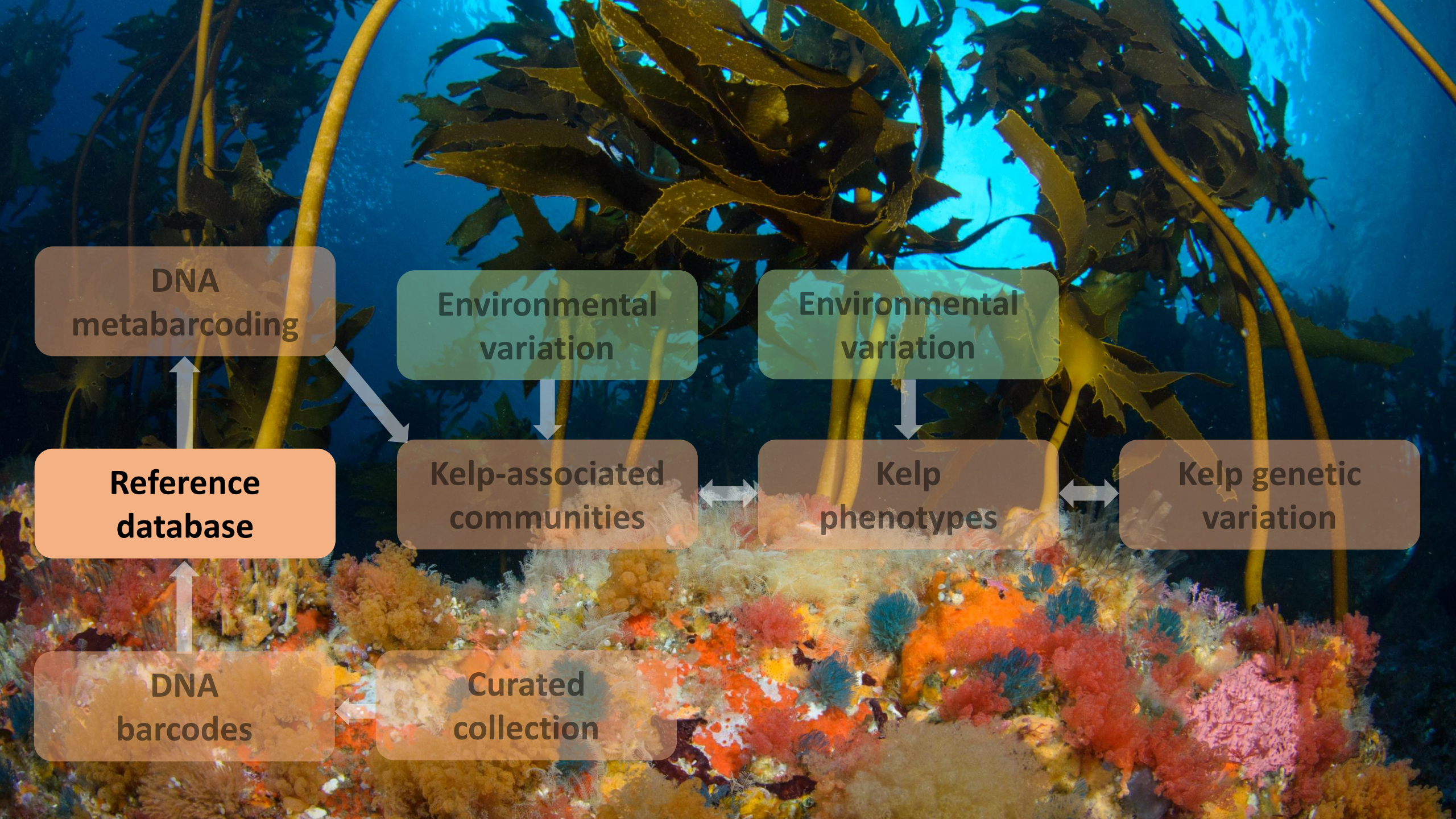
Date created: 2019-12-12 03:27 PM | Last Updated: 2021-01-25 03:04 PM

Identifier: DOI 10.17605/OSF.IO/8RDQK

Category:  Project

License: CC0 1.0 Universal 

Most comprehensive COI reference sequence database for marine Eukaryotes:
1.5M sequences, ~ 72,000 unique species (~ 27% marine species)



DNA metabarcoding

Environmental variation

Environmental variation

Reference database

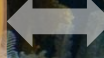
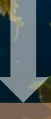
Kelp-associated communities

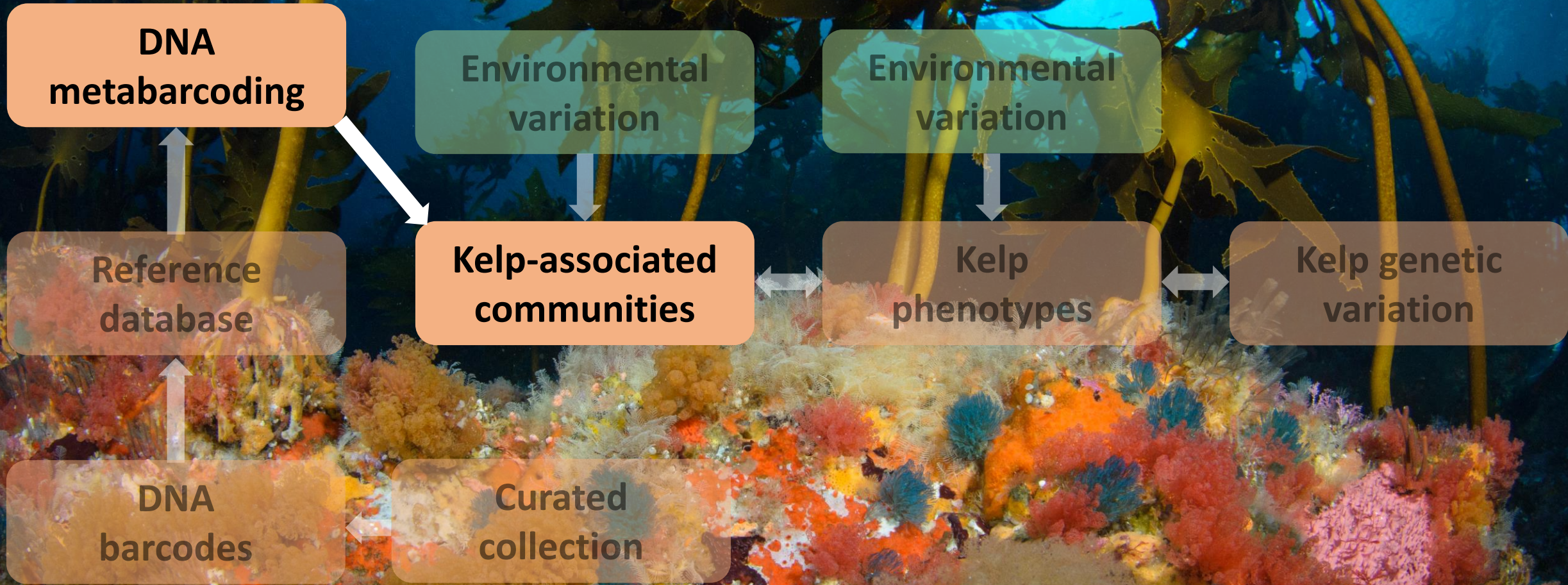
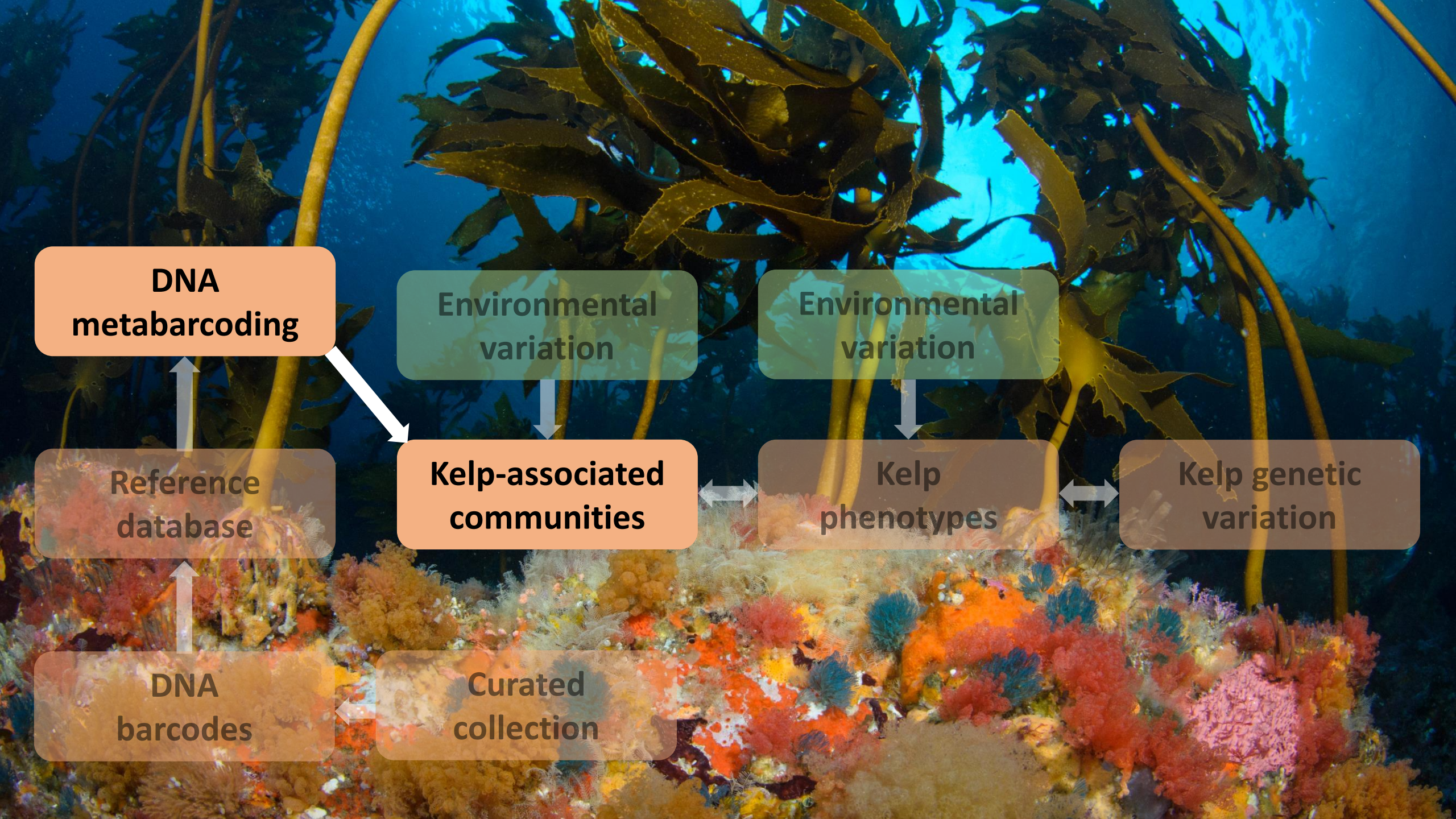
Kelp phenotypes

Kelp genetic variation

DNA barcodes

Curated collection





DOI: 10.1002/edn3.265

METHOD

Environmental DNA
Dedicated to the study and use of environmental DNA for basic and applied sciences

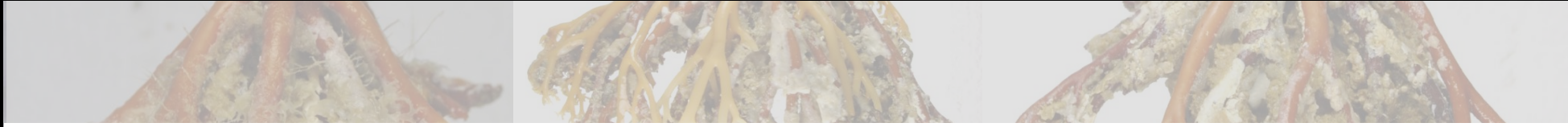
WILEY

Metabarcoding hyperdiverse kelp holdfast communities on temperate reefs: An experimental approach to inform future studies

Vanessa Arranz  | Libby Liggins  | J. David Aguirre 



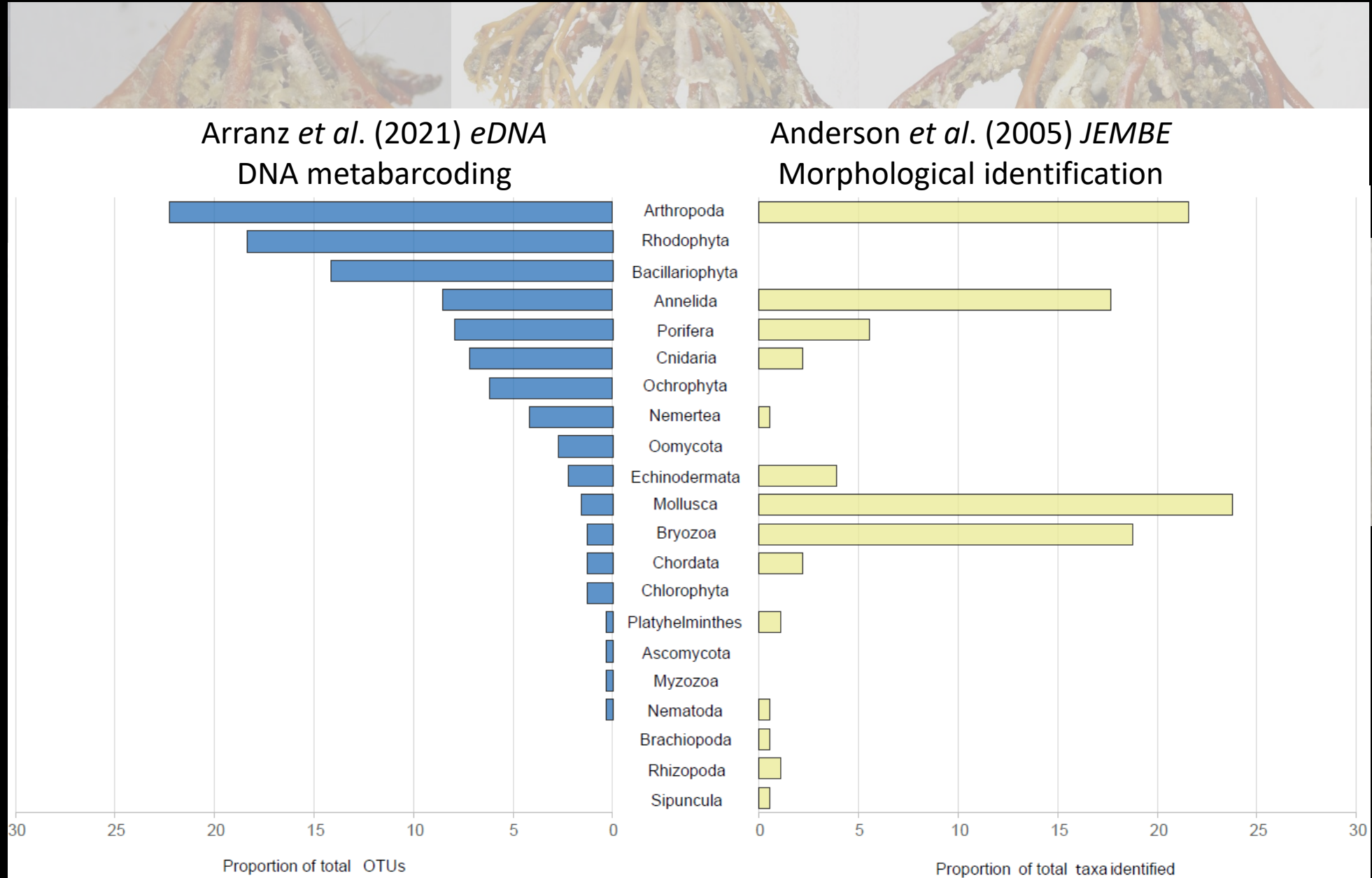
Comparing DNA metabarcoding and traditional morphological assessments



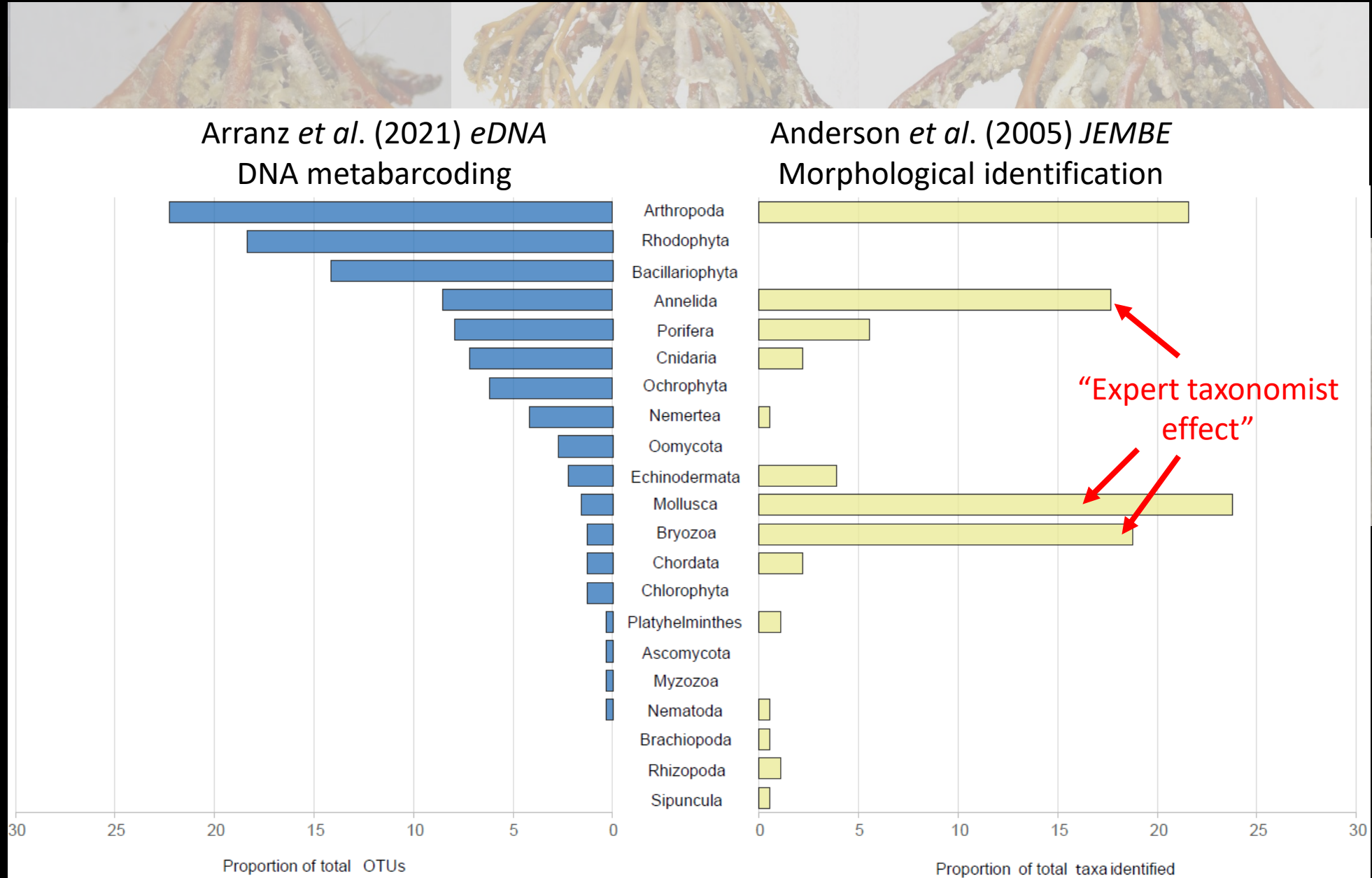
Arranz *et al.* (2021) *eDNA*
DNA metabarcoding

Anderson *et al.* (2005) *JEMBE*
Morphological identification

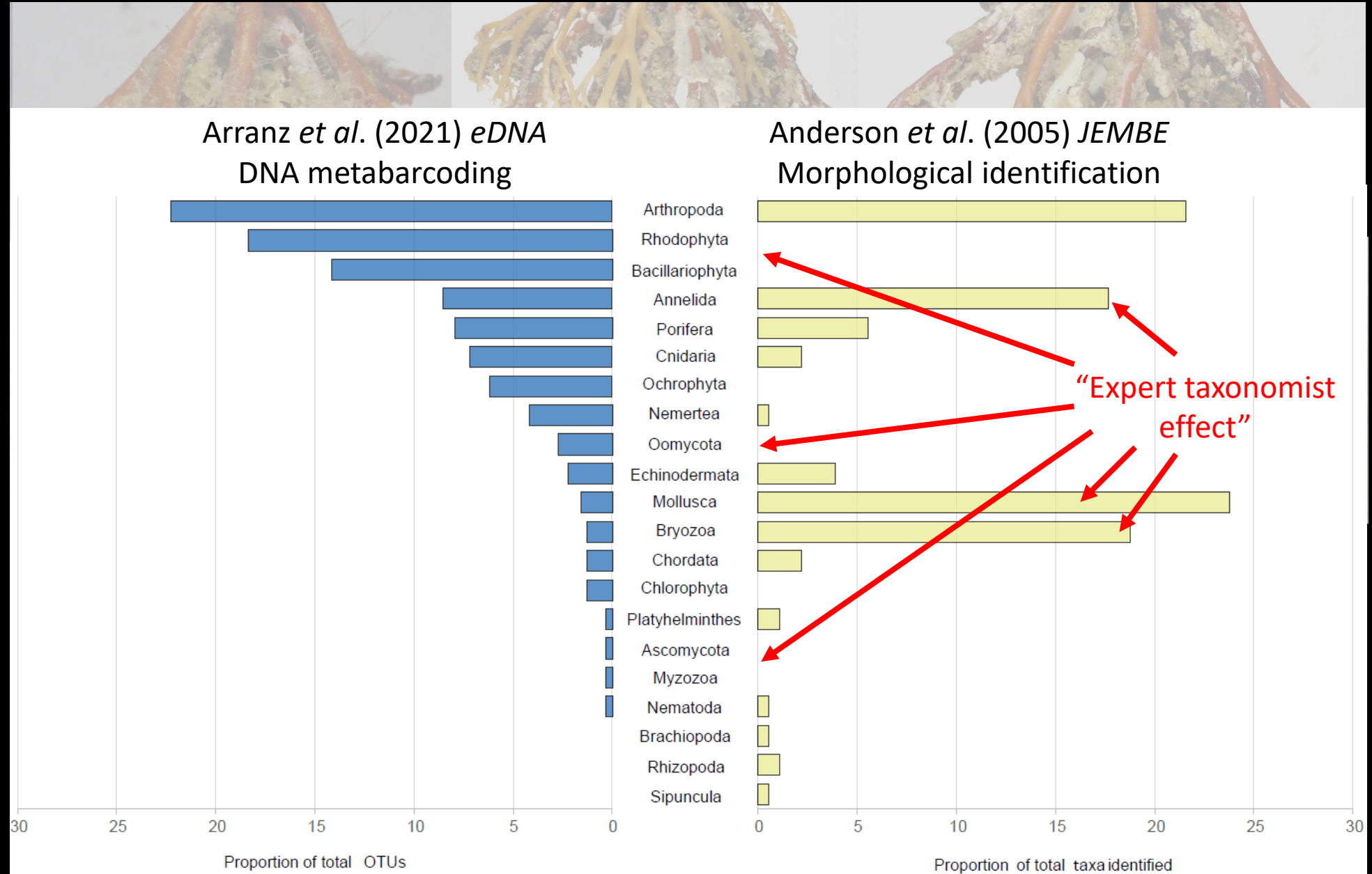
Comparing DNA metabarcoding and traditional morphological assessments



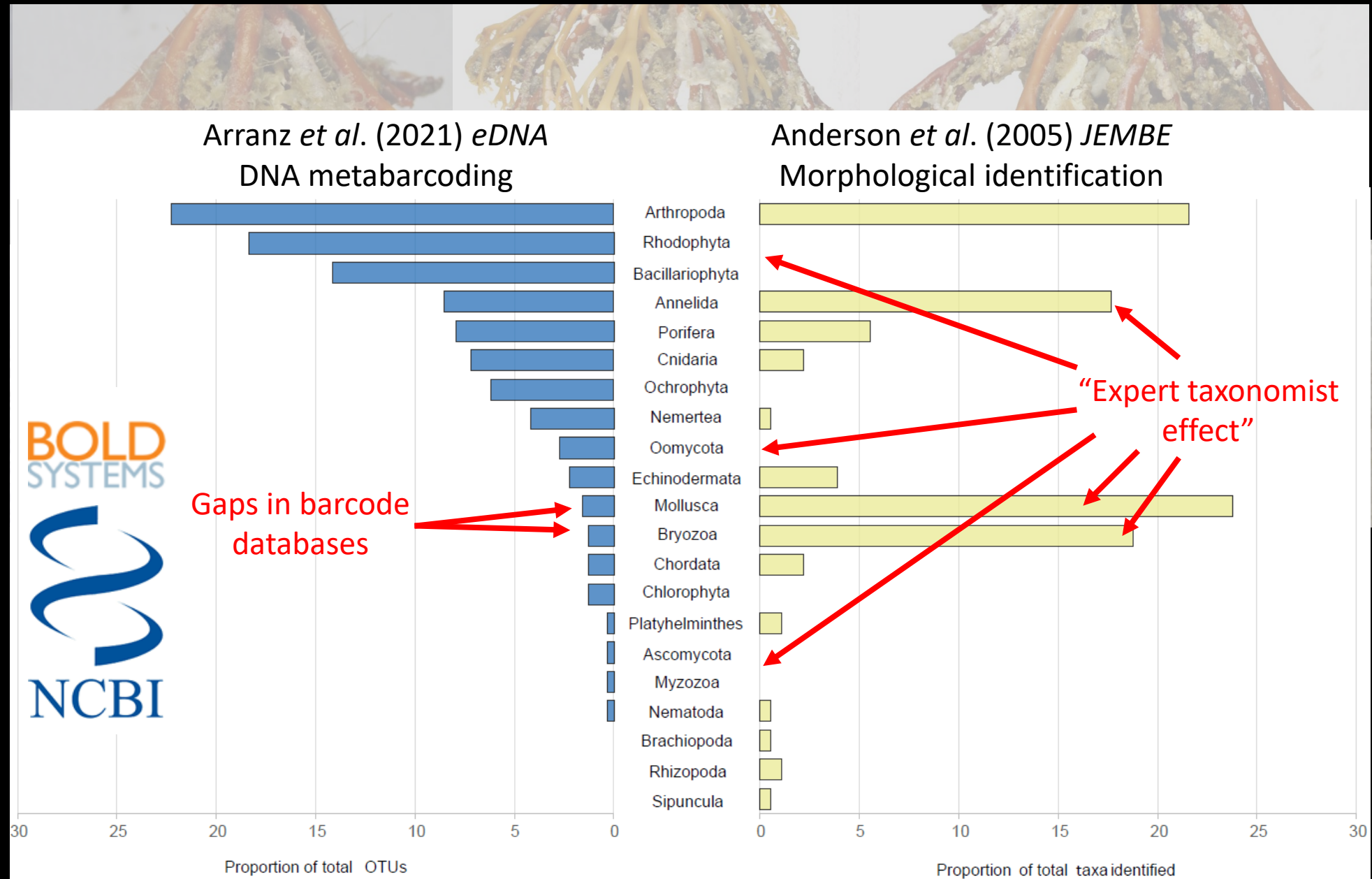
Comparing DNA metabarcoding and traditional morphological assessments

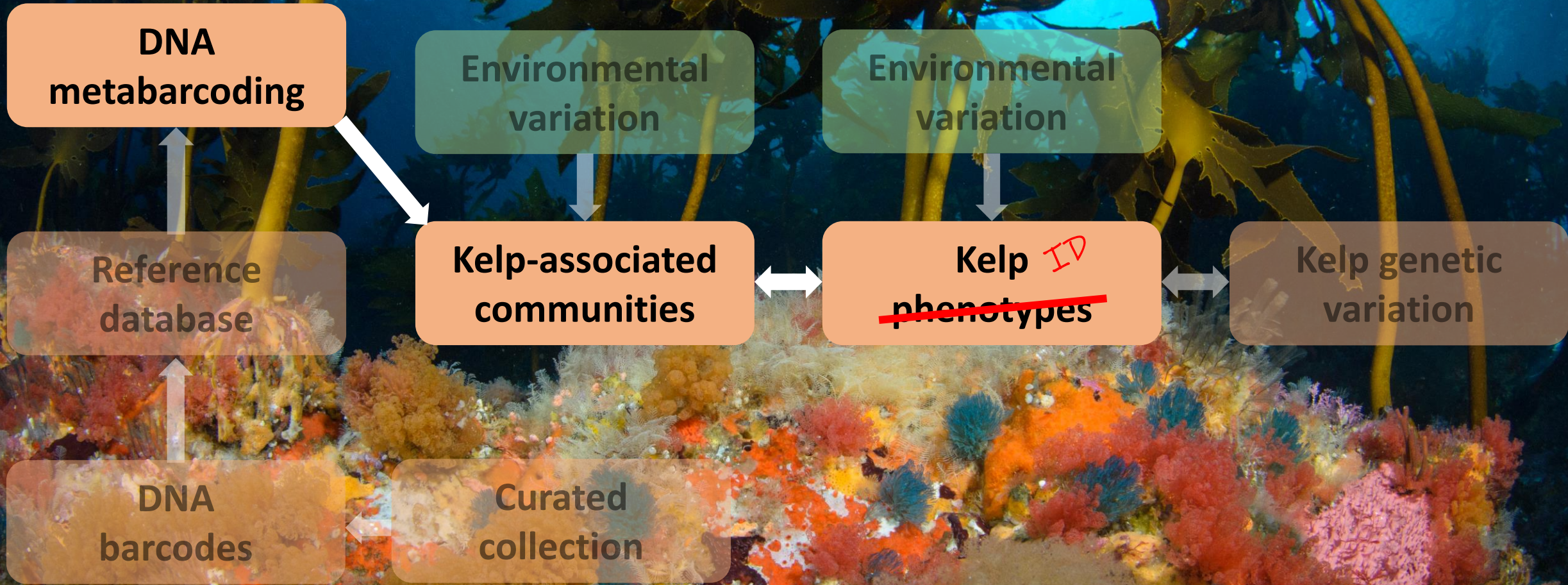
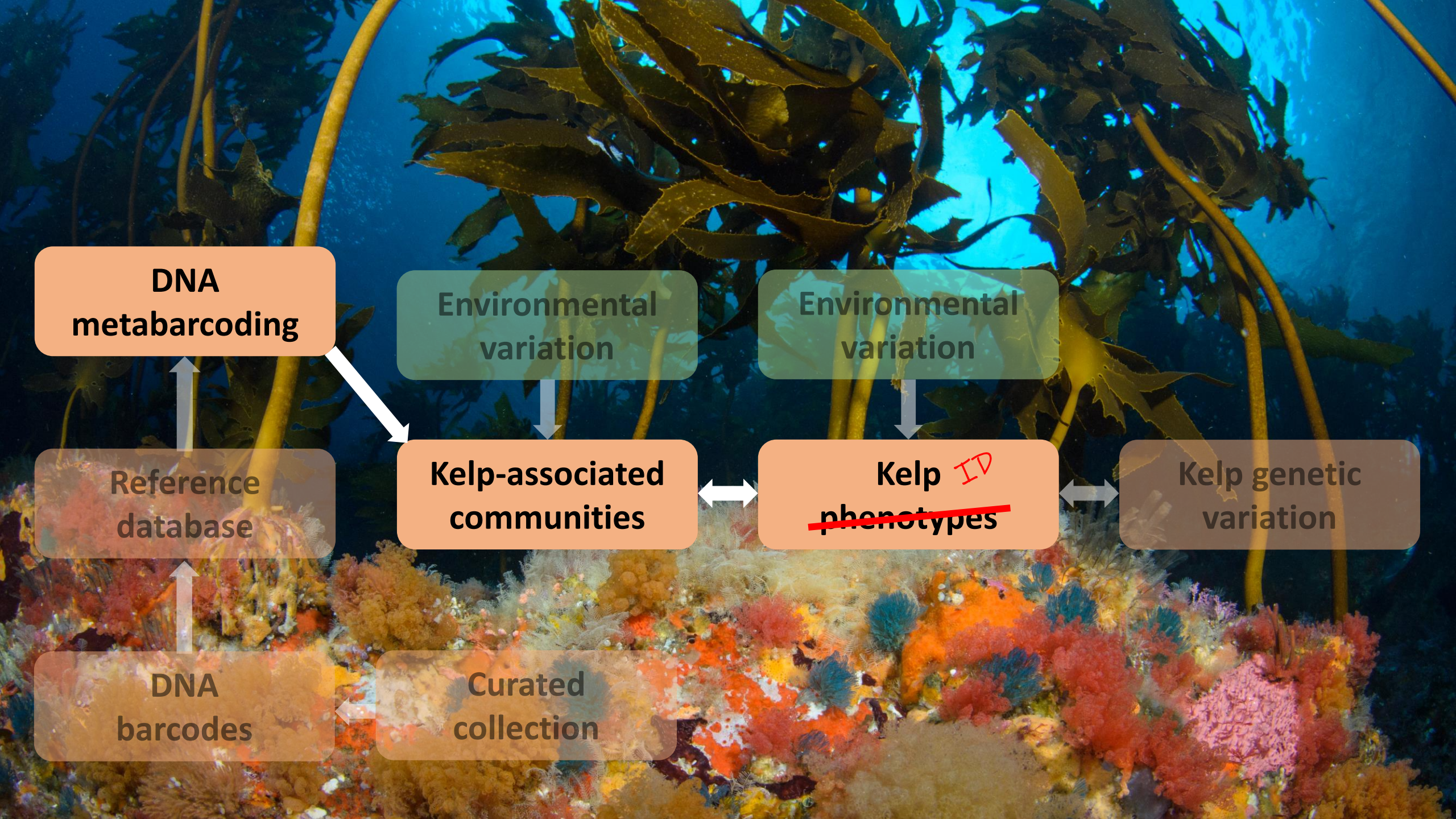


Comparing DNA metabarcoding and traditional morphological assessments

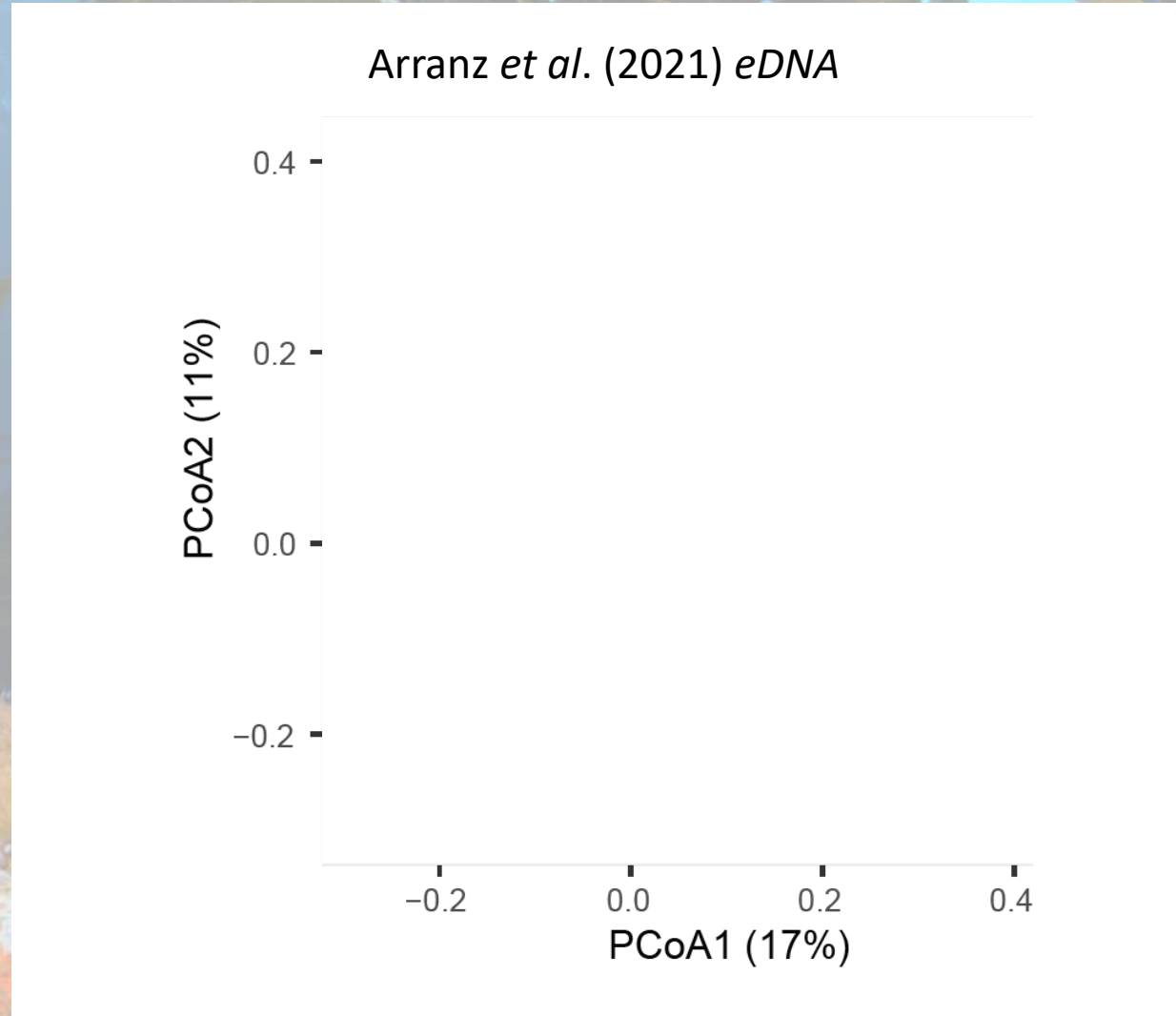


Comparing DNA metabarcoding and traditional morphological assessments

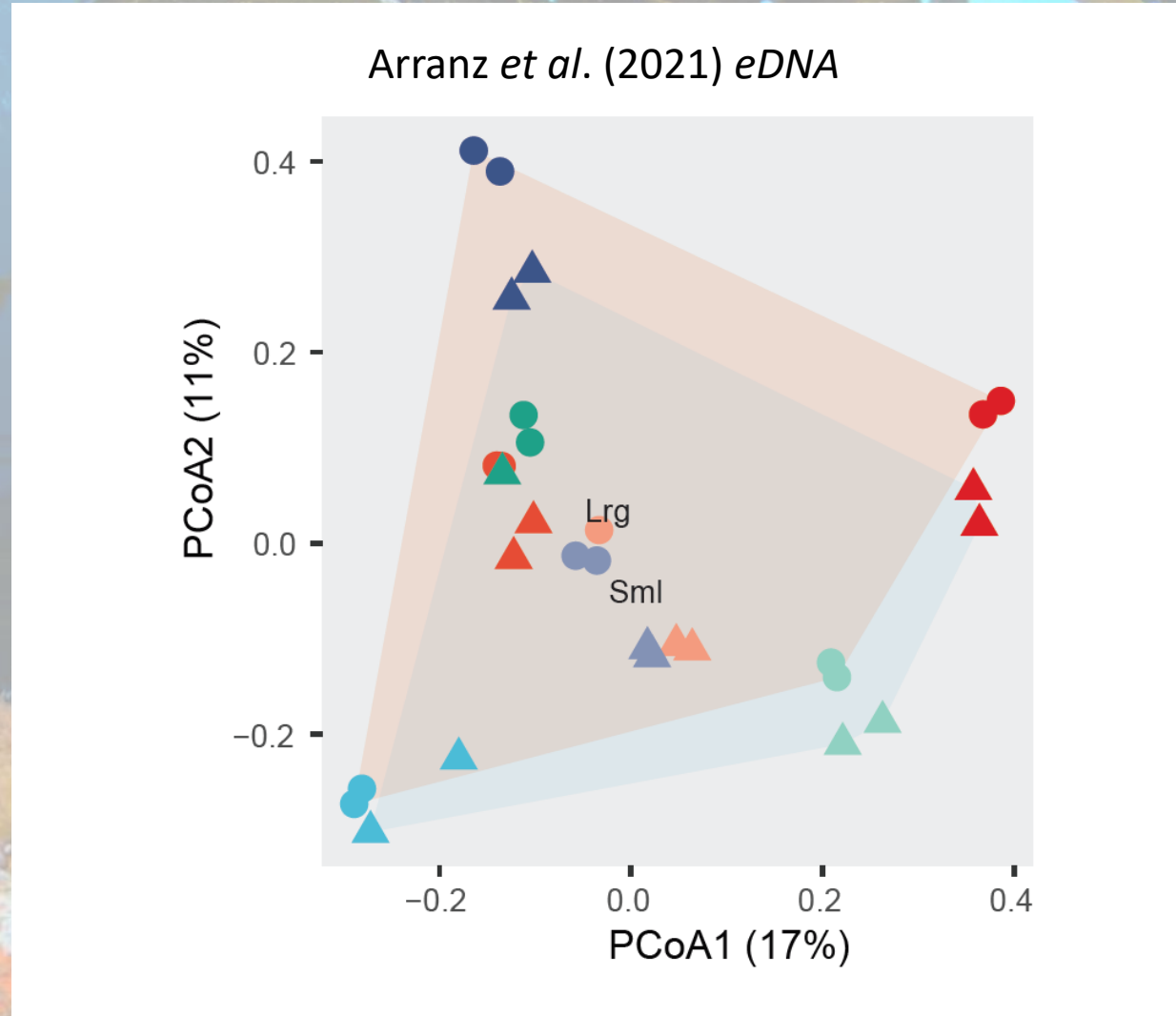


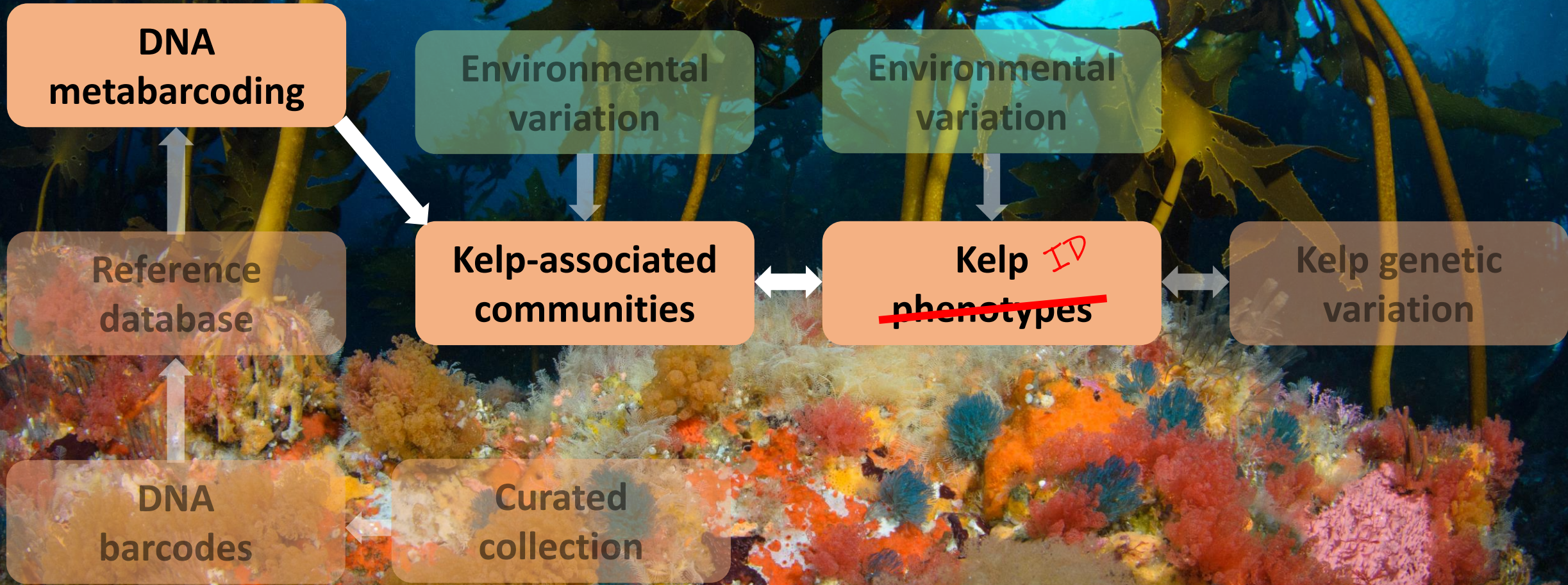
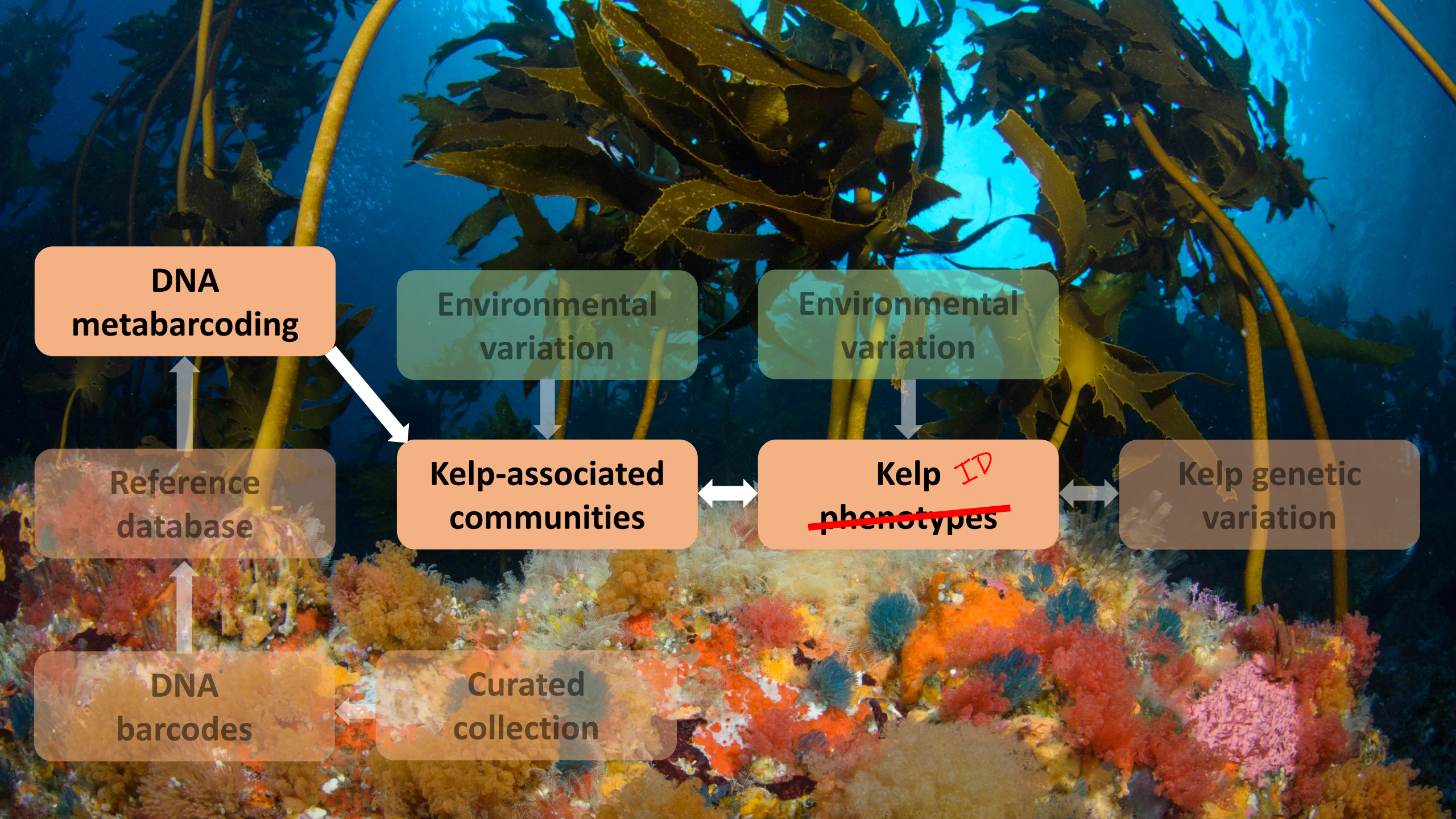


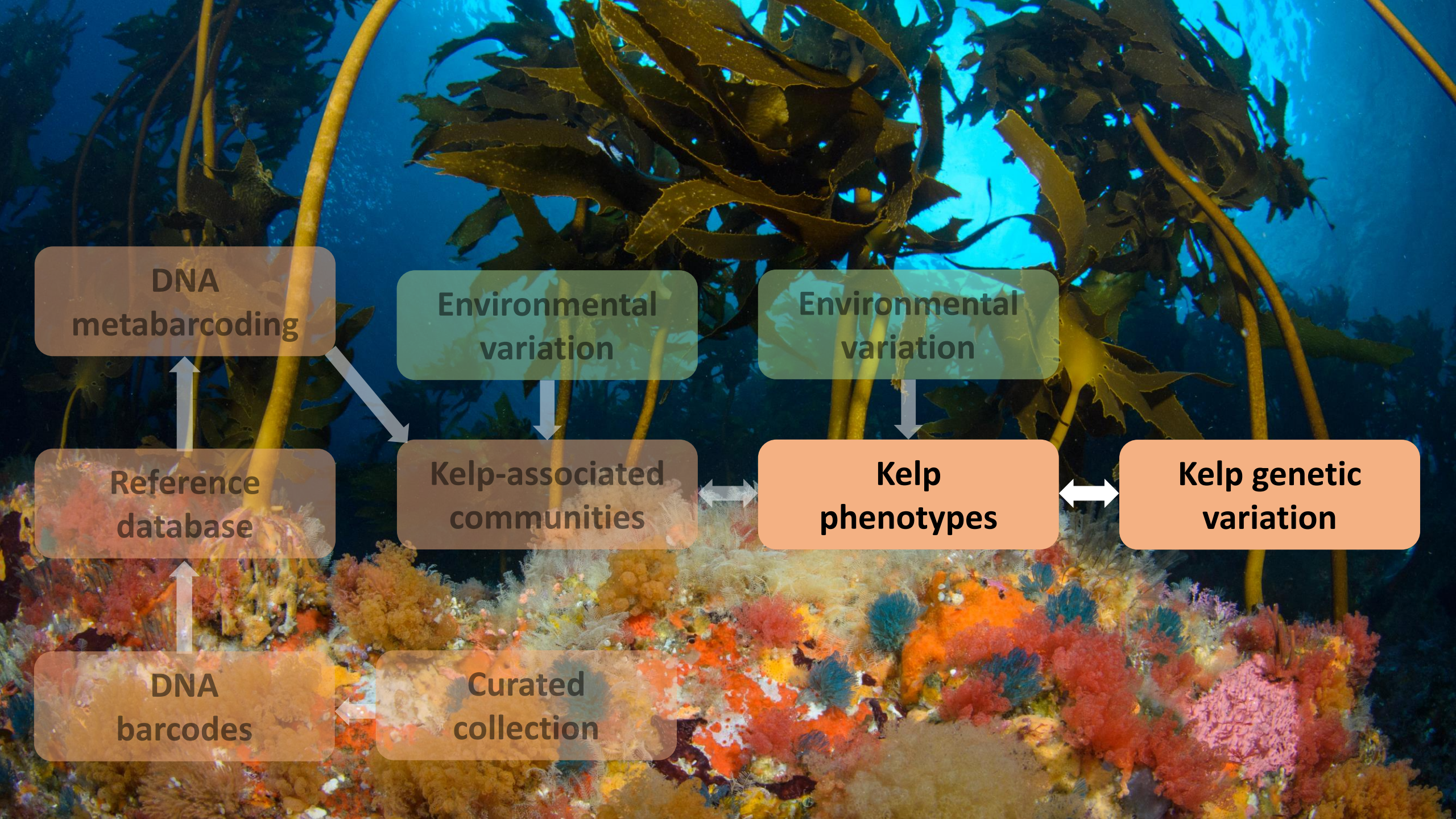
Variability in community composition strongly influenced by holdfasts ID



Variability in community composition strongly influenced by holdfasts ID







DNA
metabarcoding

Environmental
variation

Environmental
variation

Reference
database

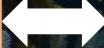
Kelp-associated
communities

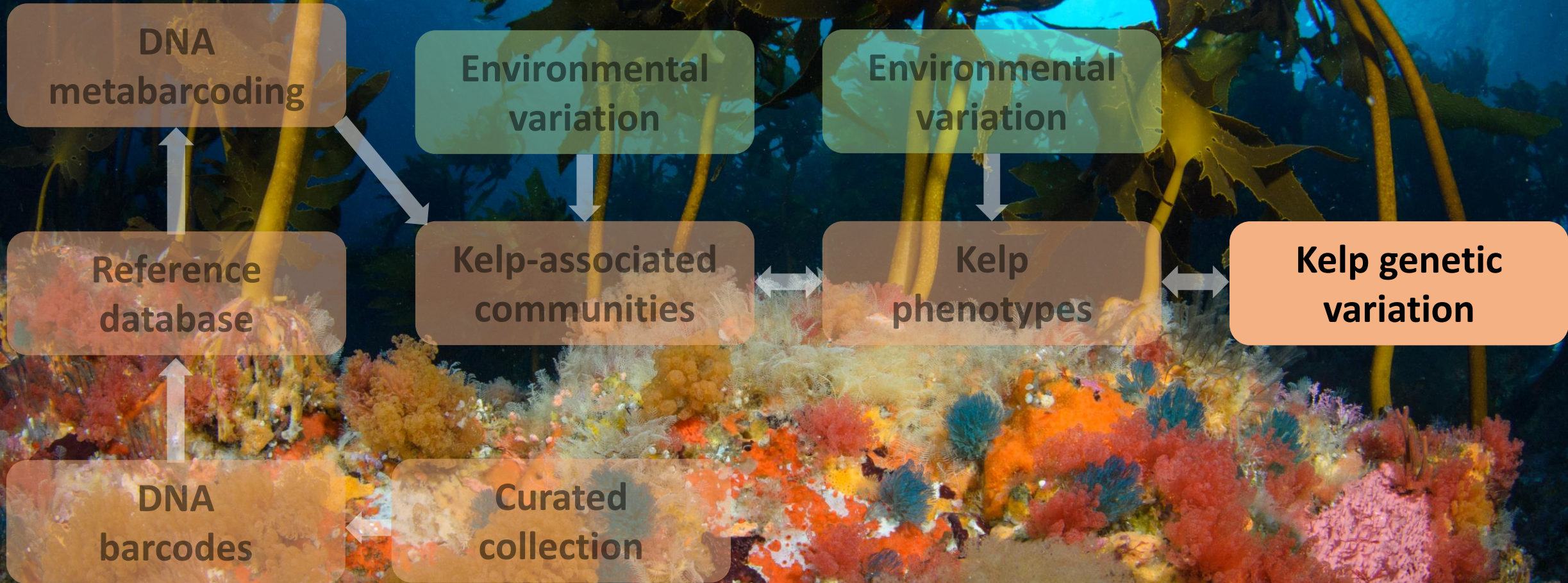
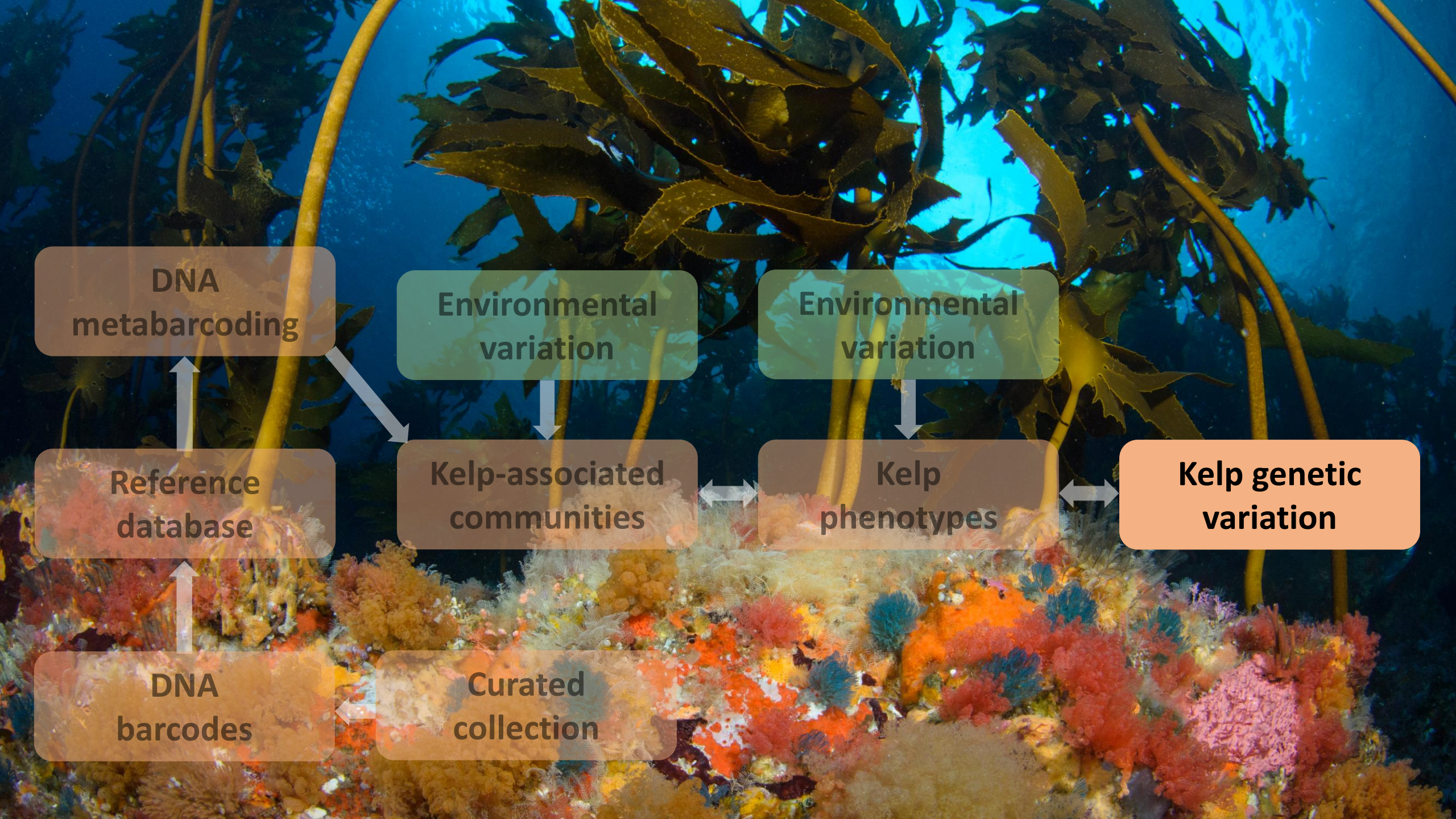
Kelp
phenotypes

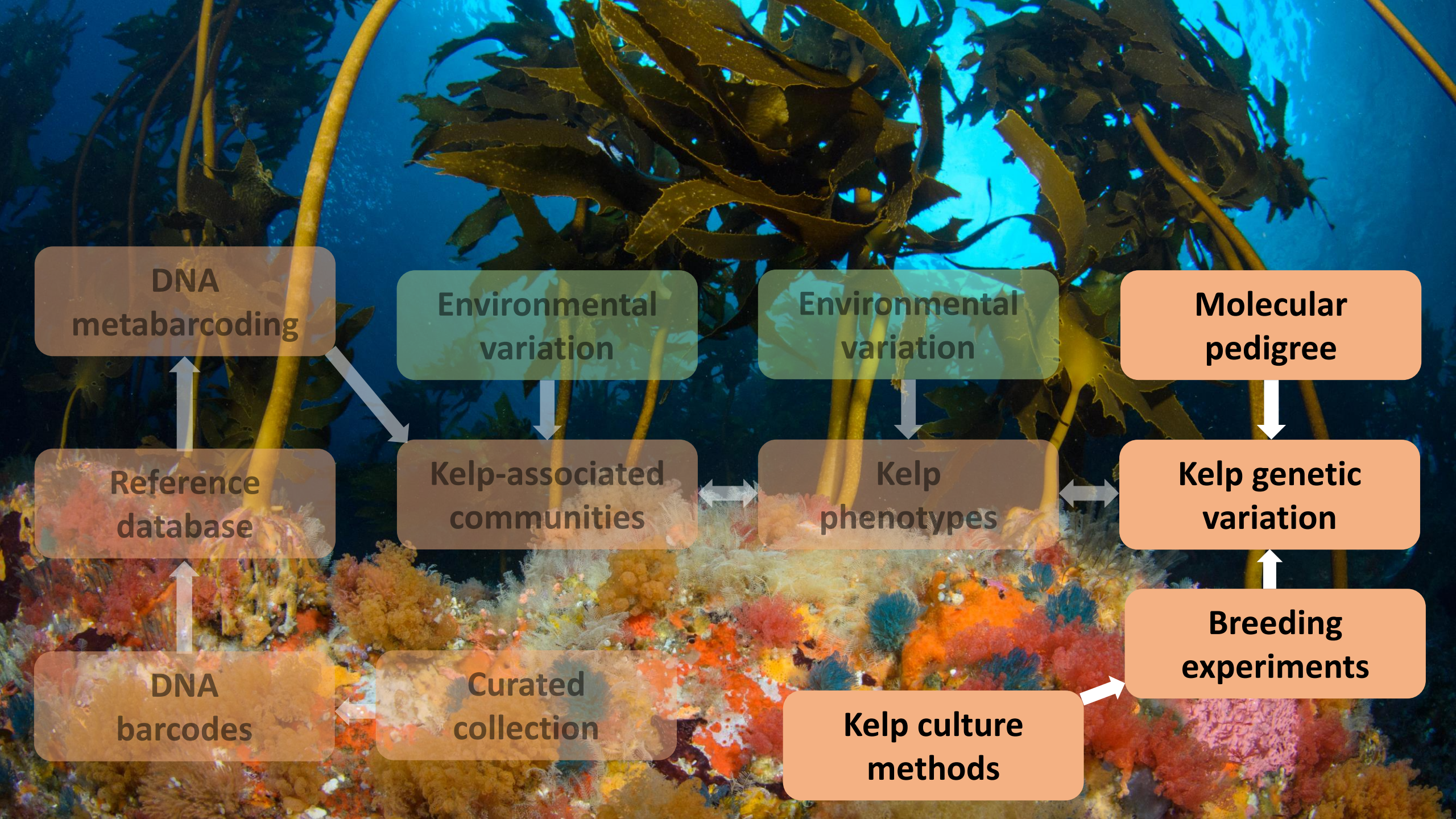
Kelp genetic
variation

DNA
barcodes

Curated
collection







DNA
metabarcoding

Environmental
variation

Environmental
variation

Molecular
pedigree

Reference
database

Kelp-associated
communities

Kelp
phenotypes

Kelp genetic
variation

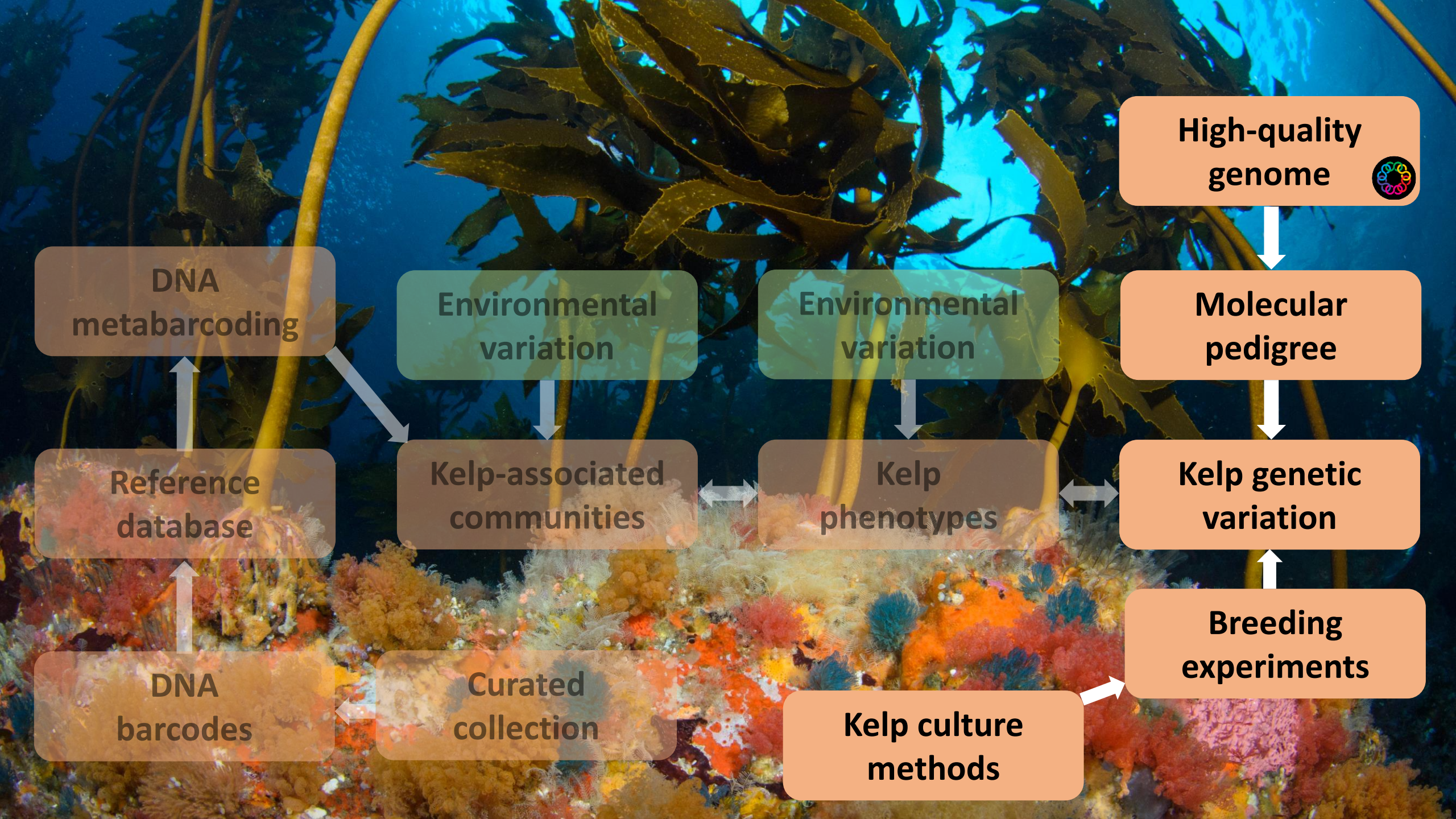
DNA
barcodes

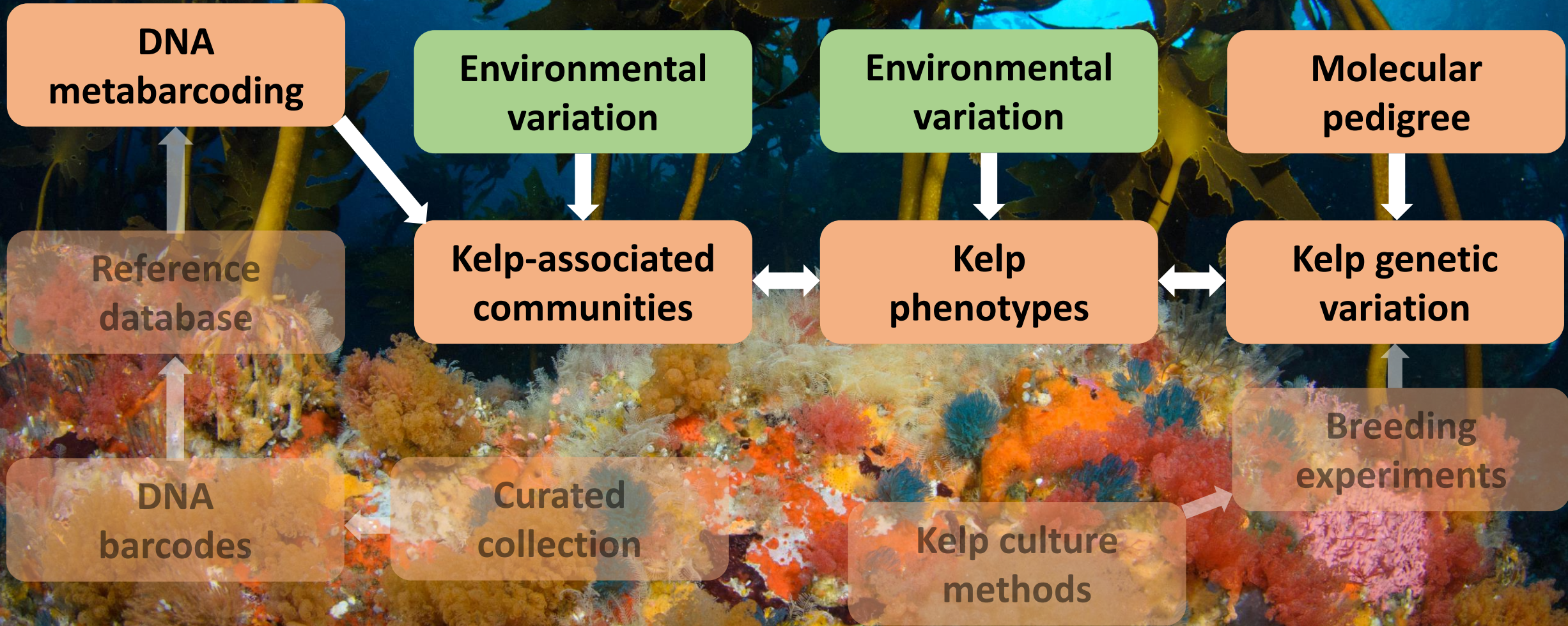
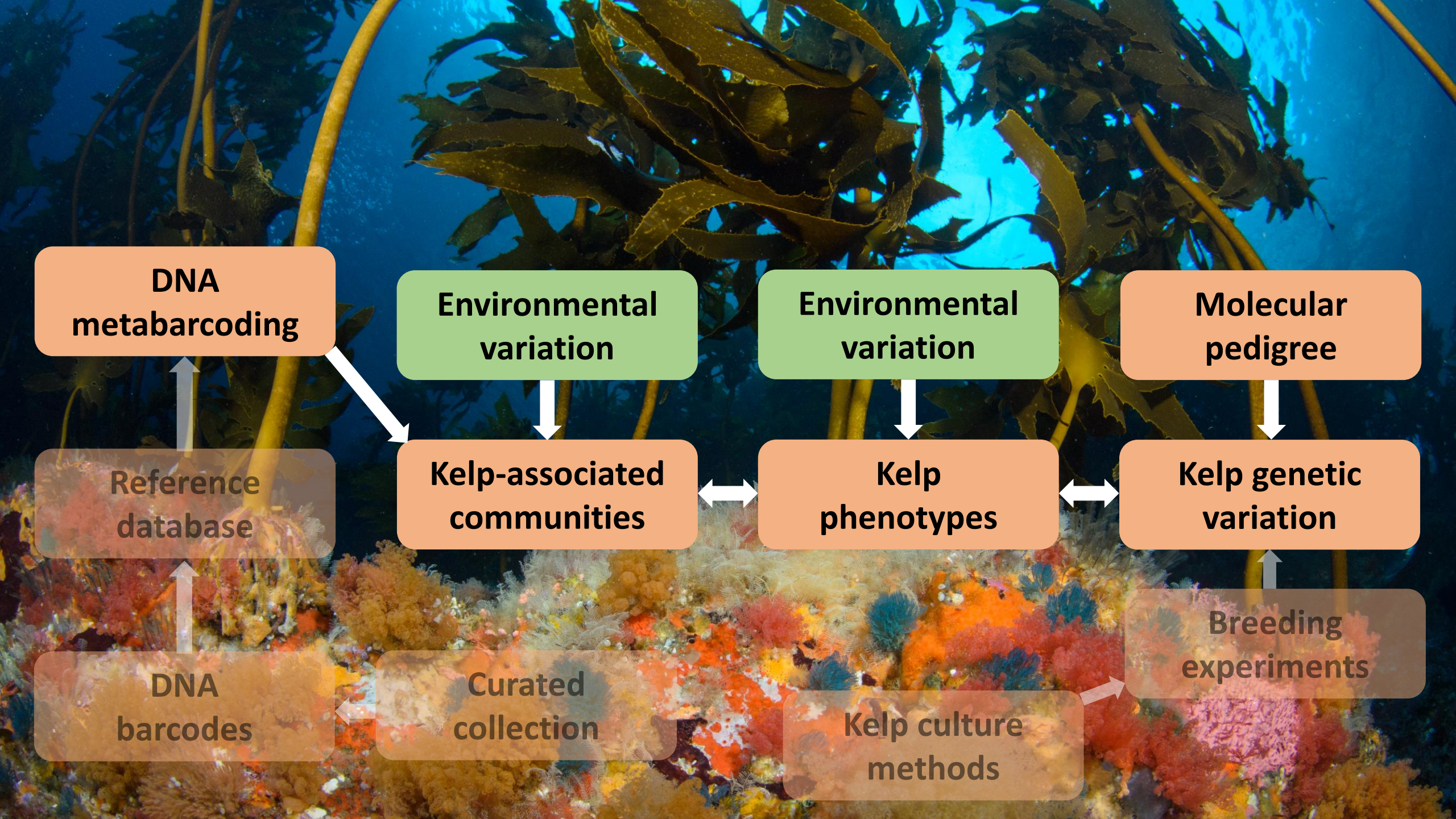
Curated
collection

Kelp culture
methods

Breeding
experiments







Quantifying relatedness in wild populations

30 kelp randomly sampled from a 100m² area of reef

MTB30
MTB29
MTB28
MTB27
MTB26
MTB25
MTB24
MTB23
MTB22
MTB21
MTB20
MTB19
MTB09
MTB17
MTB18
MTB14
MTB16
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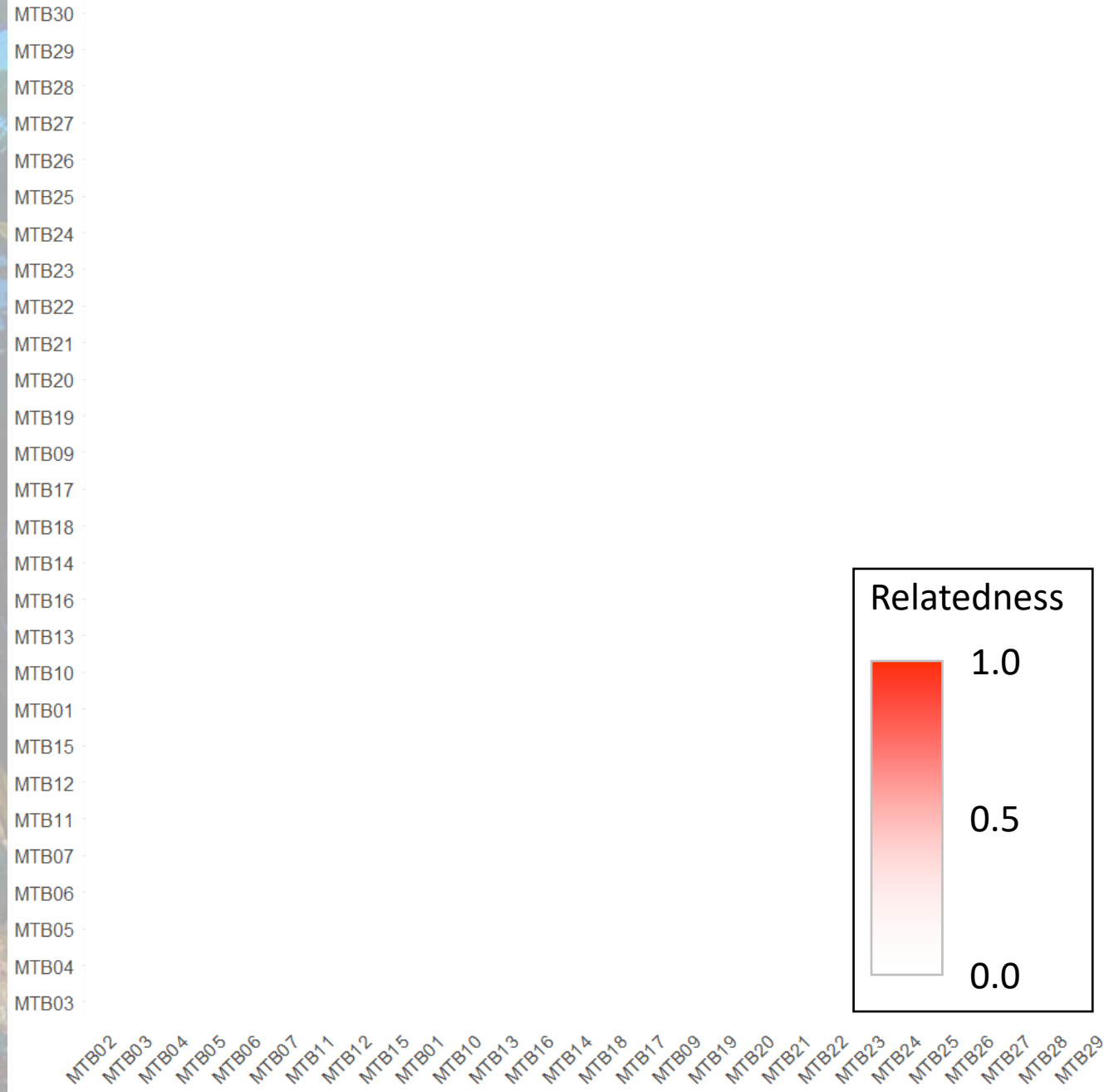
Quantifying relatedness in wild populations

30 kelp randomly sampled from a 100m² area of reef

Genotype-by-sequencing resulted in 5,319 SNP from 2,564 loci

Determined kinship using genotype-by-sequencing with depth adjustment¹

Genomic relatedness matrix estimated using G_5 algorithm¹



¹Dodds *et al.* (2015) *BMC Genomics*

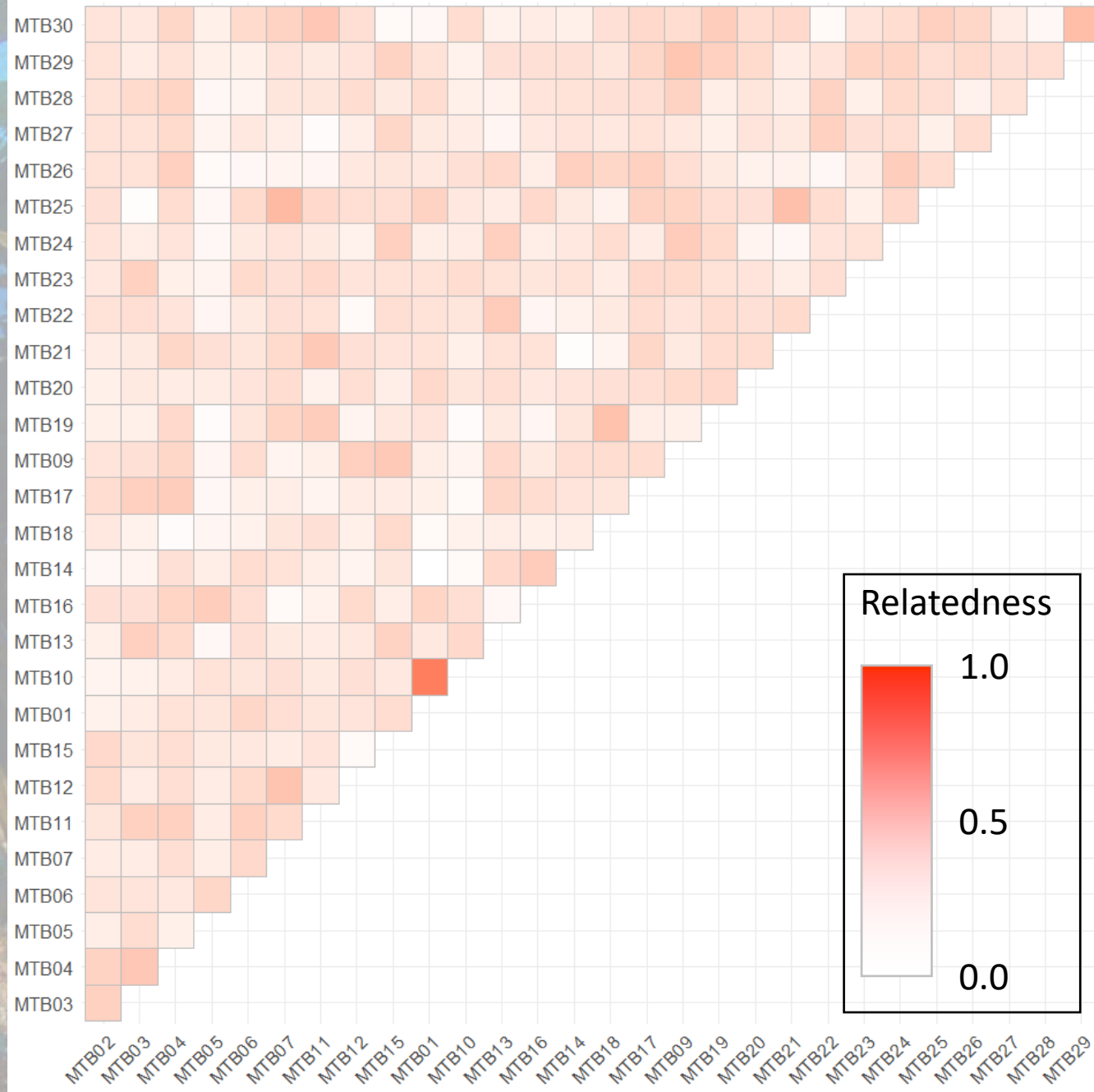
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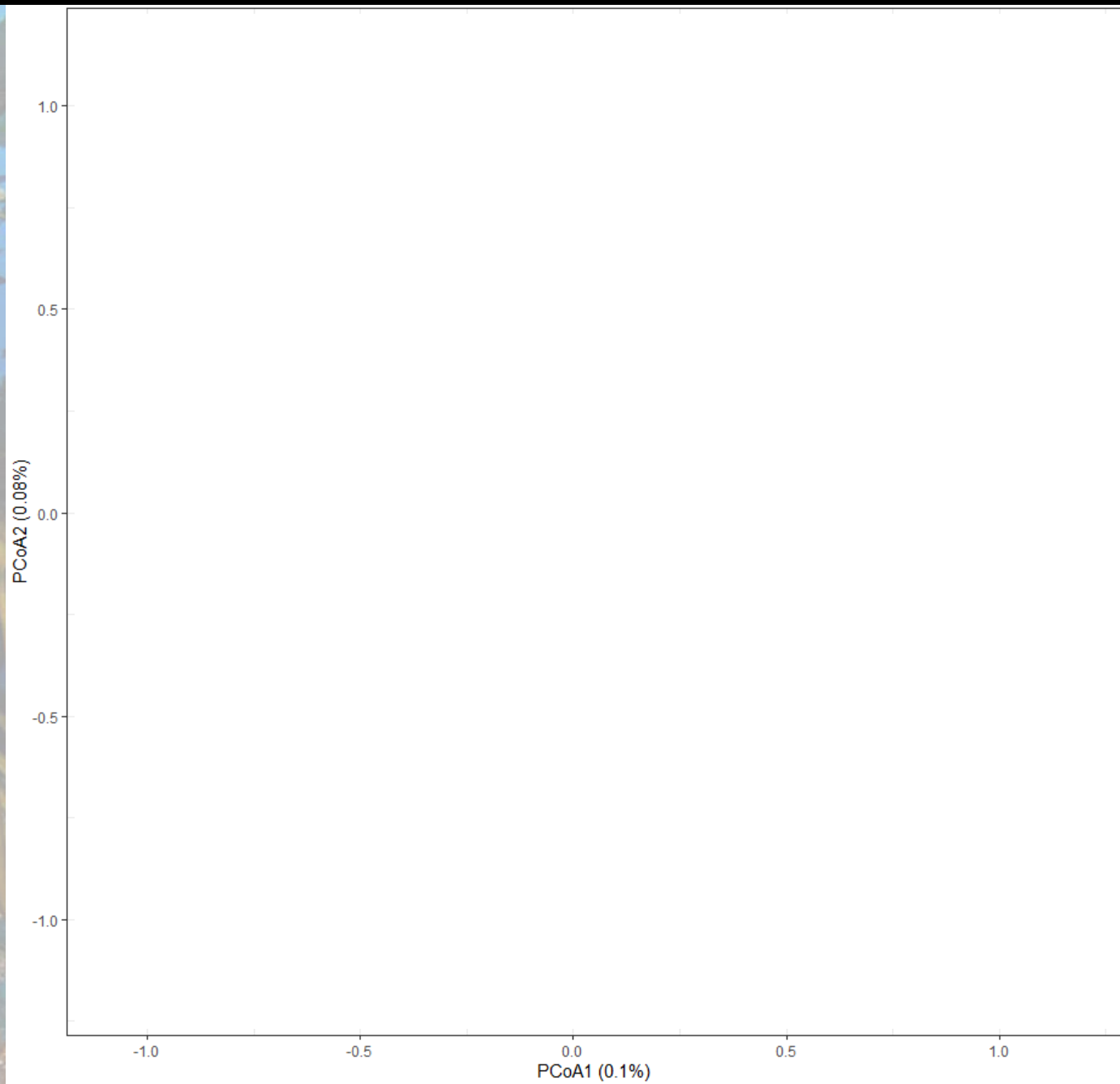
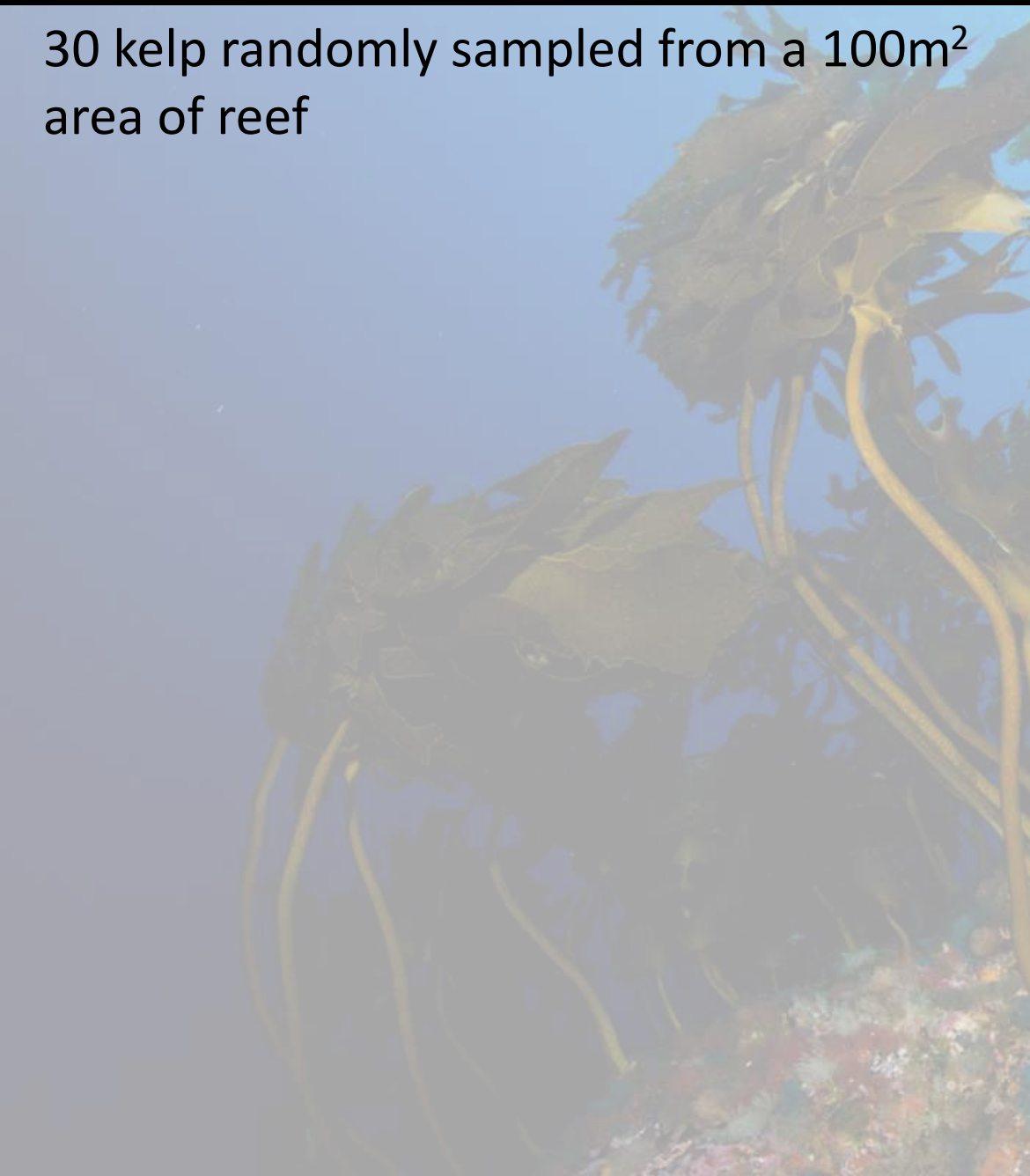
Genomic relatedness matrix estimated using G₅ algorithm¹



¹Dodds *et al.* (2015) *BMC Genomics*

Quantifying holdfast community composition

30 kelp randomly sampled from a 100m² area of reef



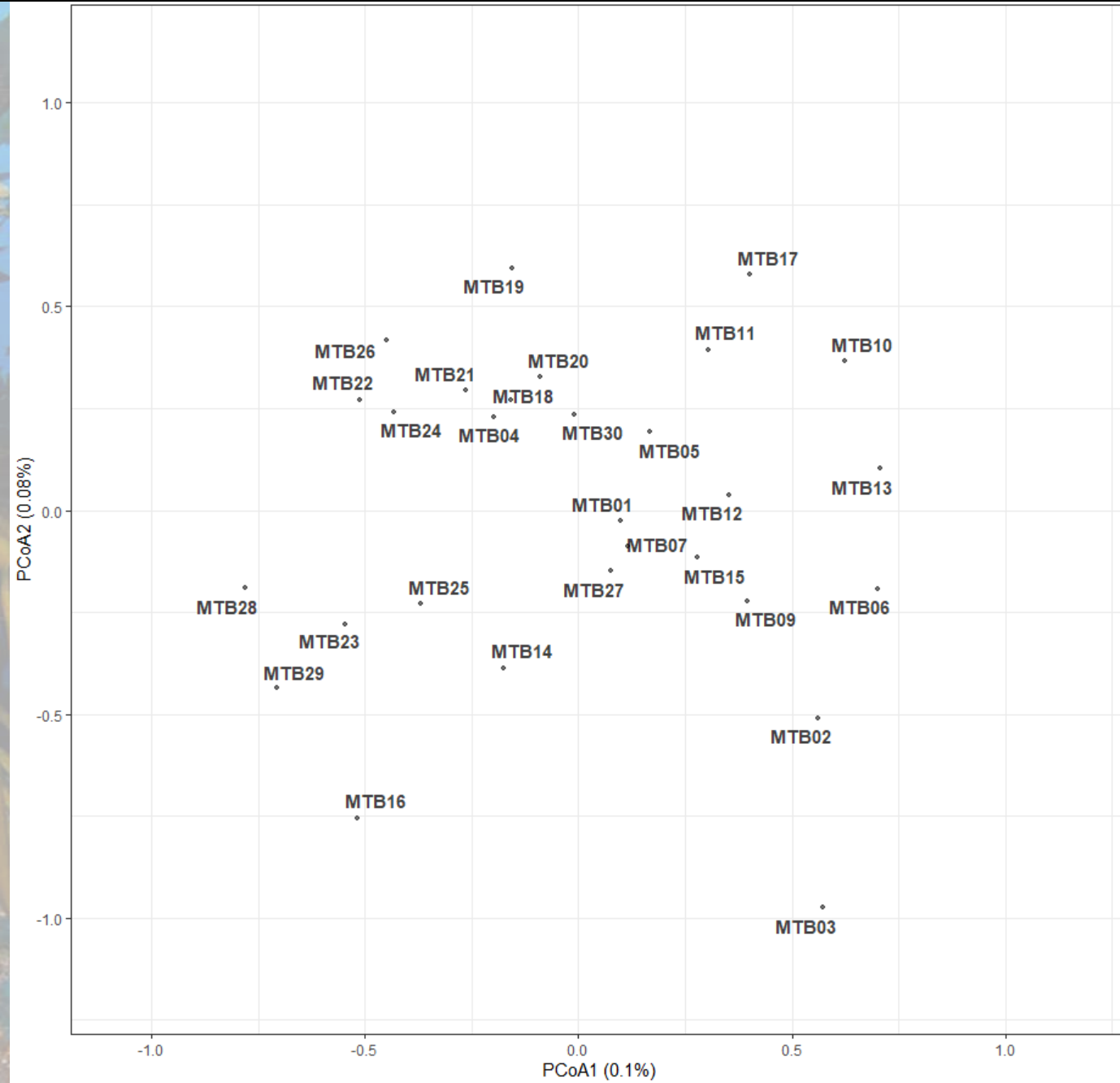
Quantifying holdfast community composition

30 kelp randomly sampled from a 100m² area of reef

Samples processed as in Arranz *et al.* (2021) *eDNA*

OTUs taxonomically assigned using the MARES reference sequence database¹

Quantified the principal coordinate axes of variability in community composition²



¹Arranz *et al.* (2020) *Sci. data*

²*vegan* R package

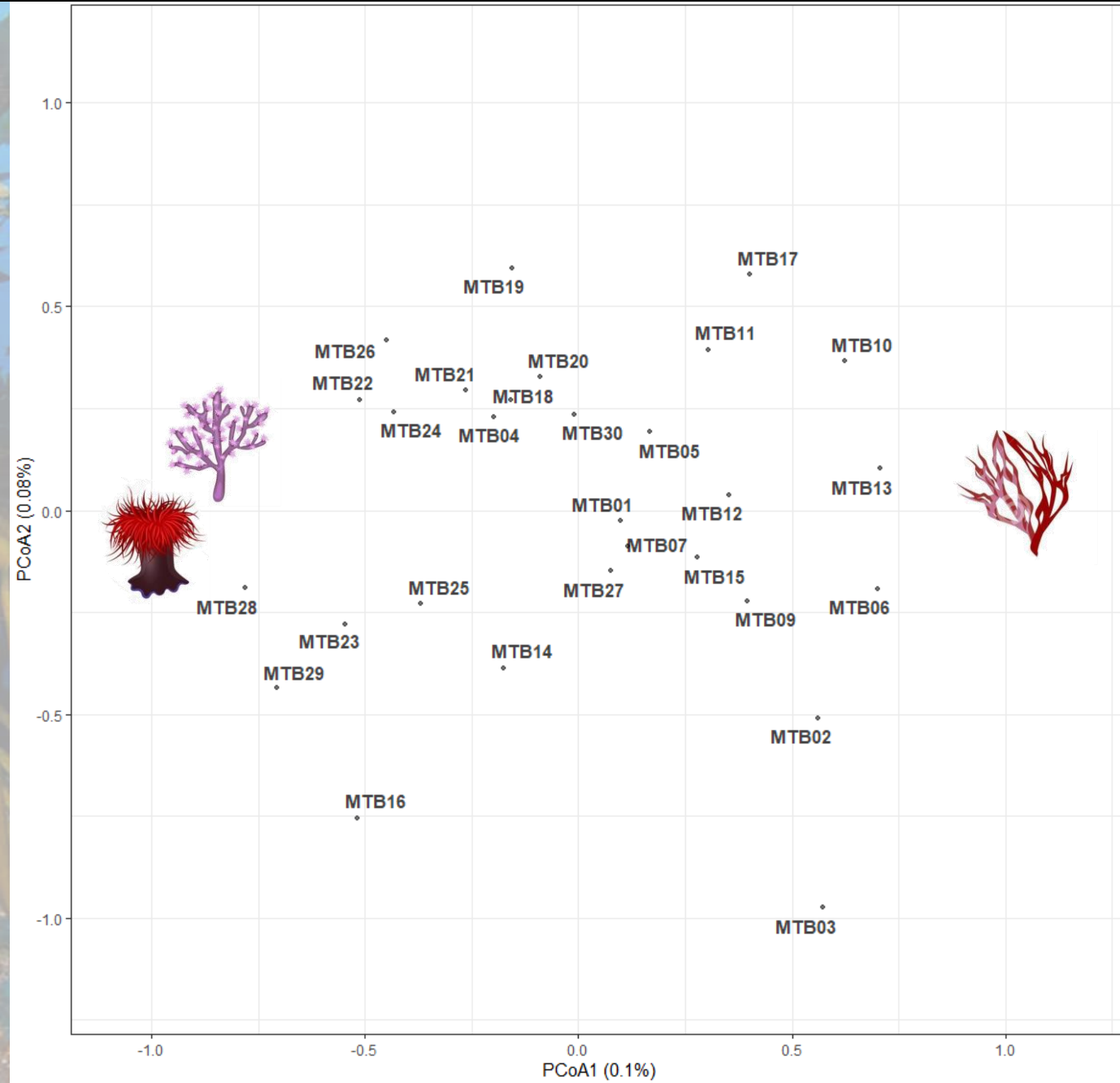
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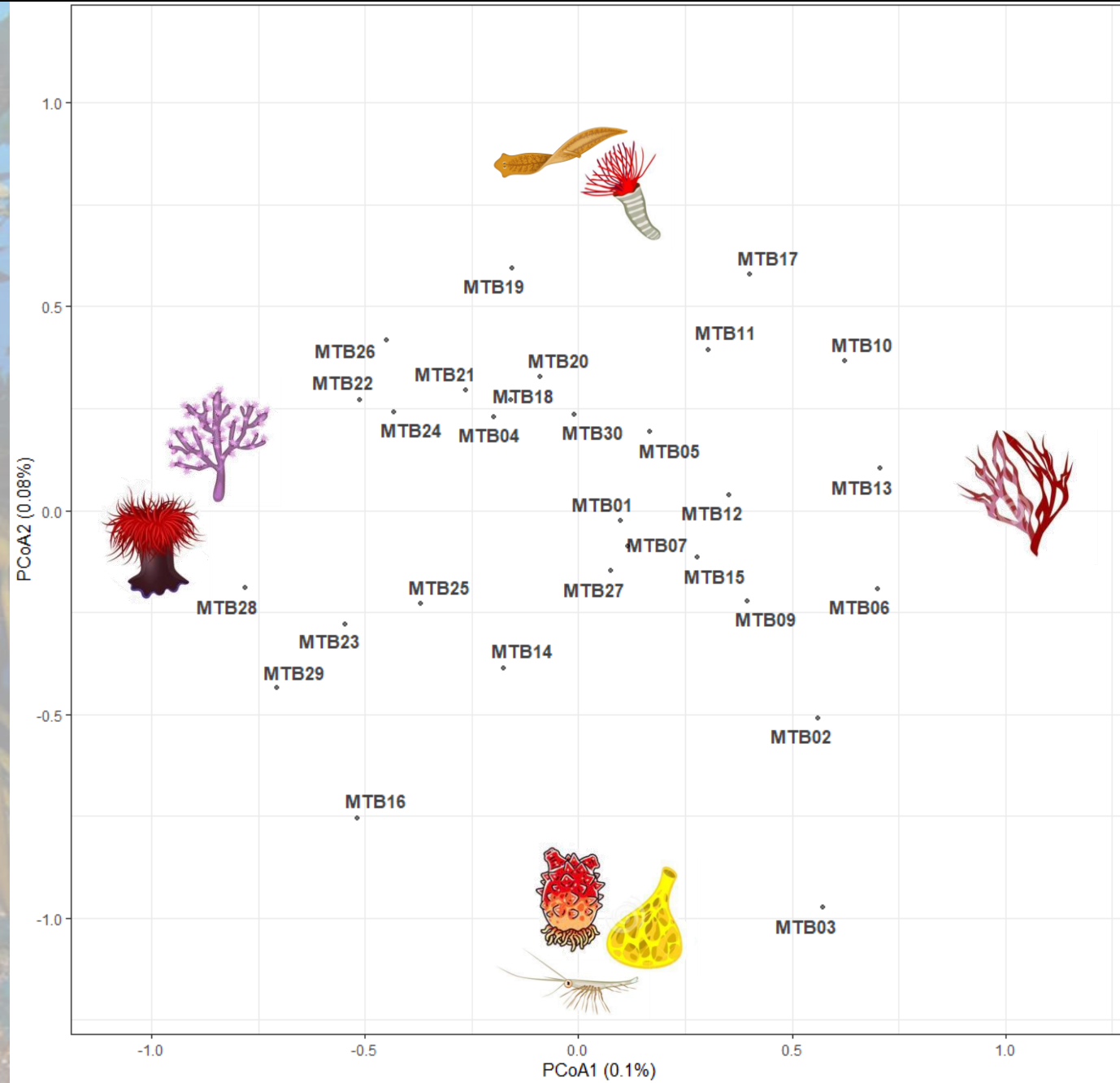
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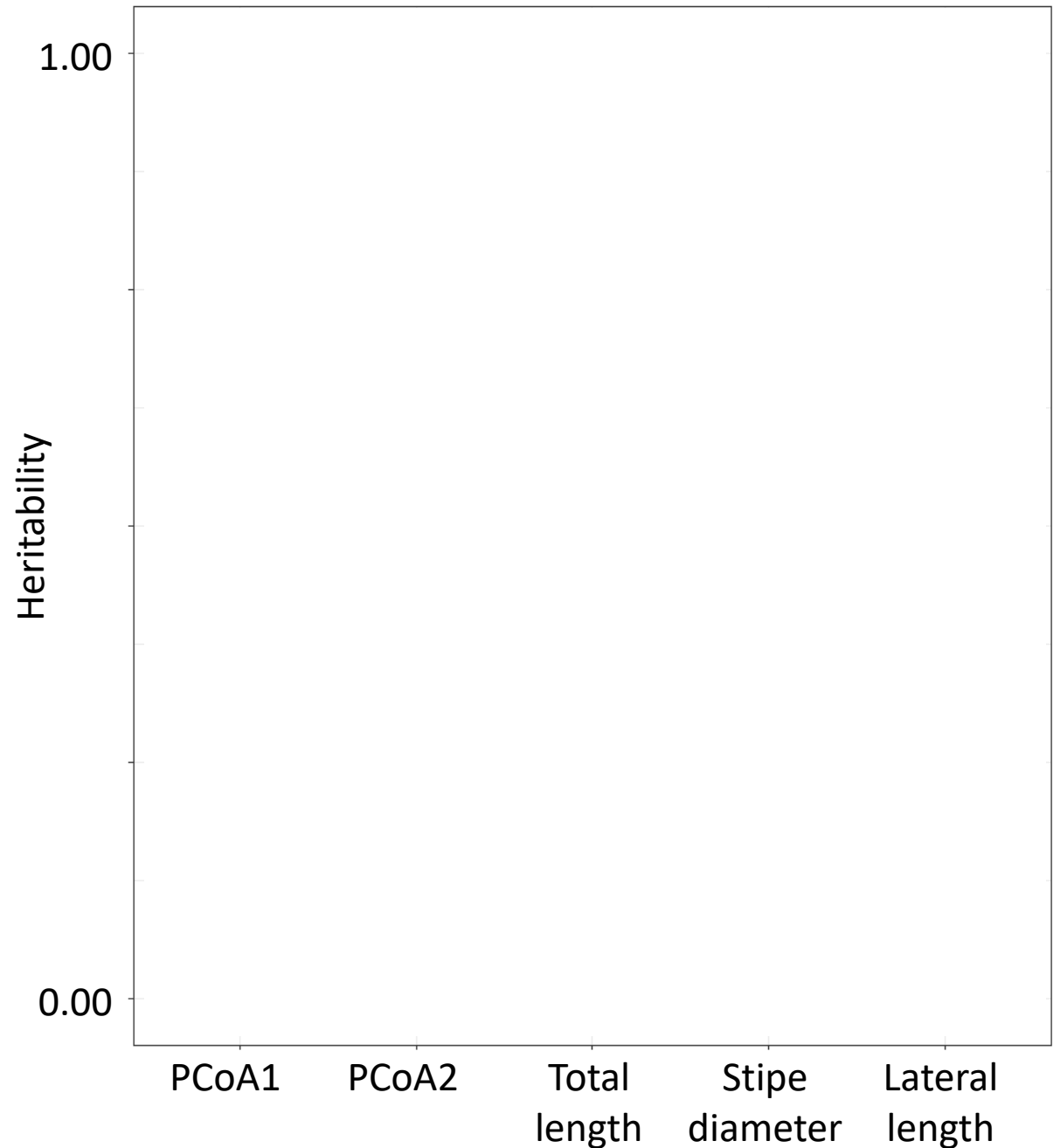
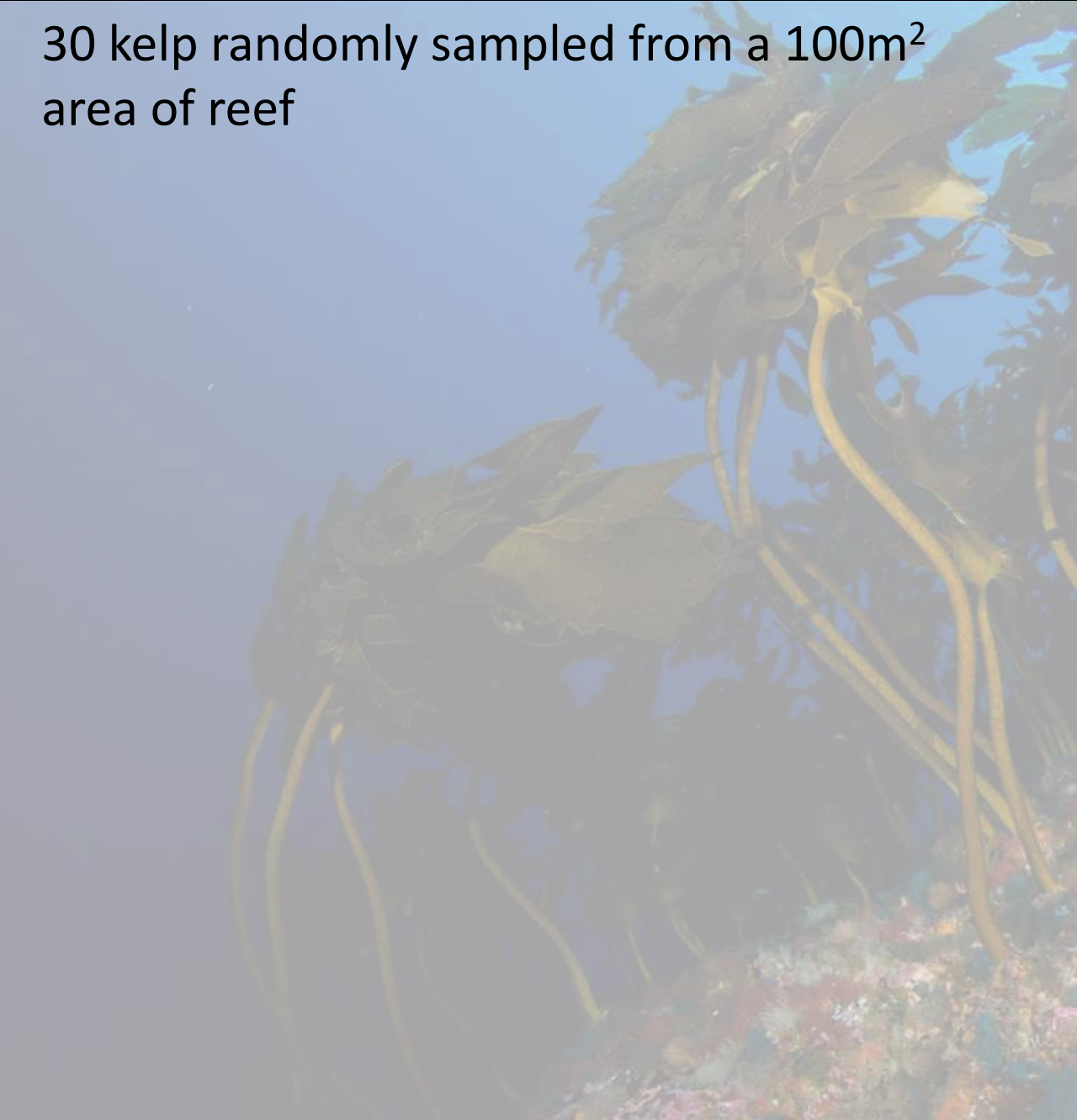


¹Arranz *et al.* (2020) *Sci. data*

²*vegan* R package

Heritable kelp phenotypes and repeatable community composition

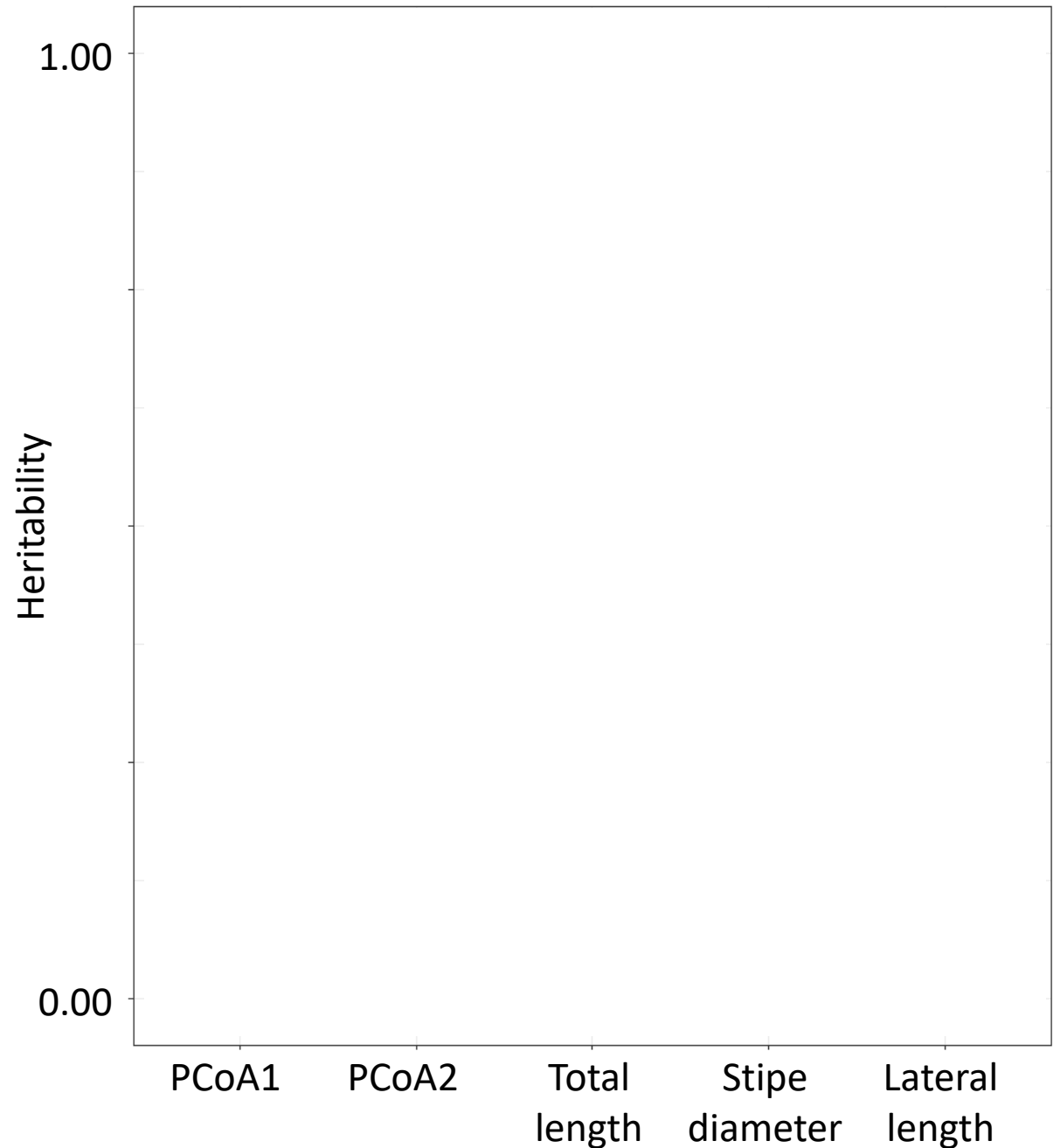
30 kelp randomly sampled from a 100m² area of reef



Heritable kelp phenotypes and repeatable community composition

30 kelp randomly sampled from a 100m² area of reef

Measured total length, stipe diameter and lateral length



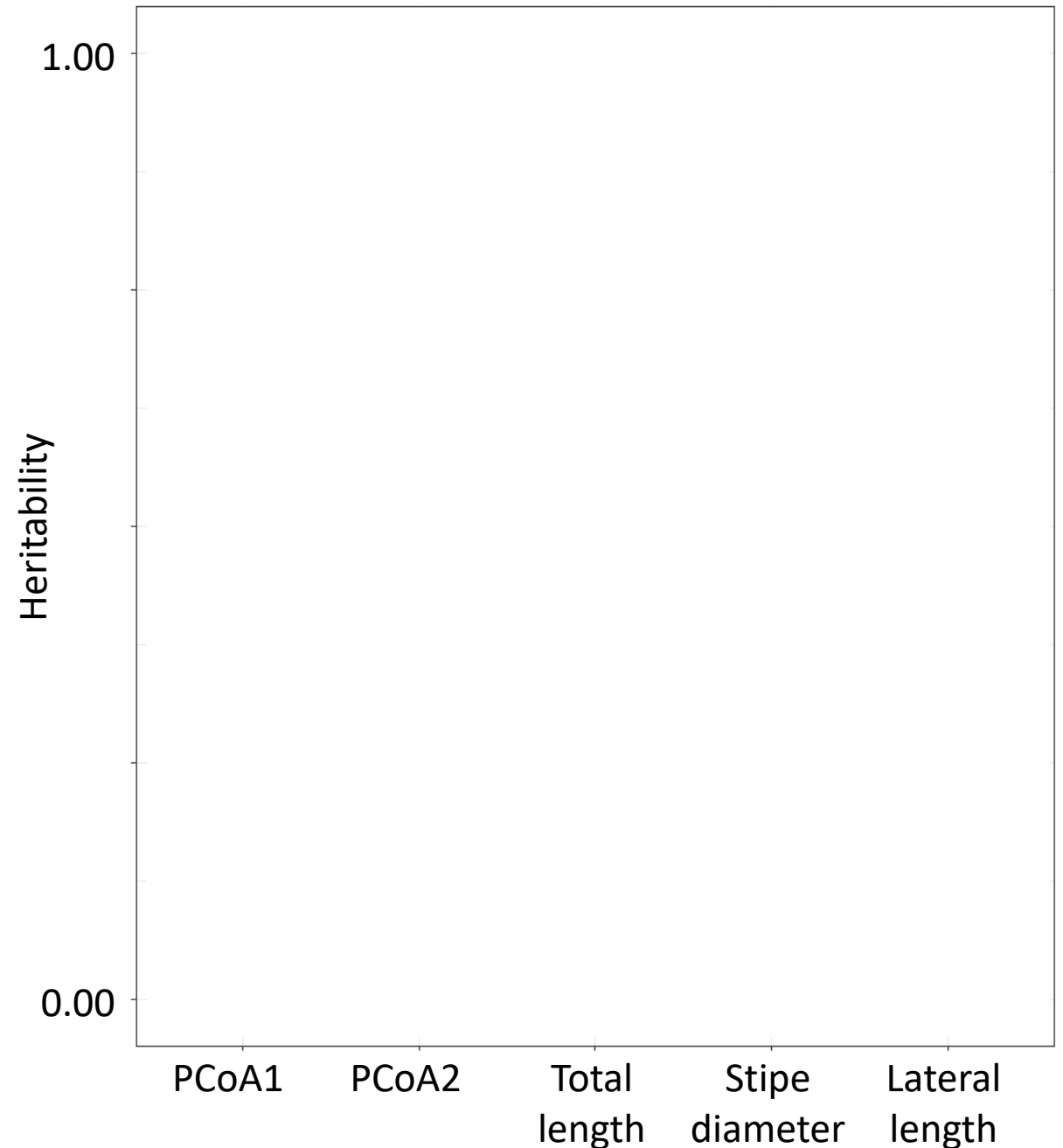
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Multivariate linear mixed model¹ to partition phenotypic variation in kelp morphology and community composition

$$\text{Heritability} = \frac{\text{Genetic variation}}{\text{Phenotypic variation}}$$



¹Hadfield (2010) *J. Stat. Software*

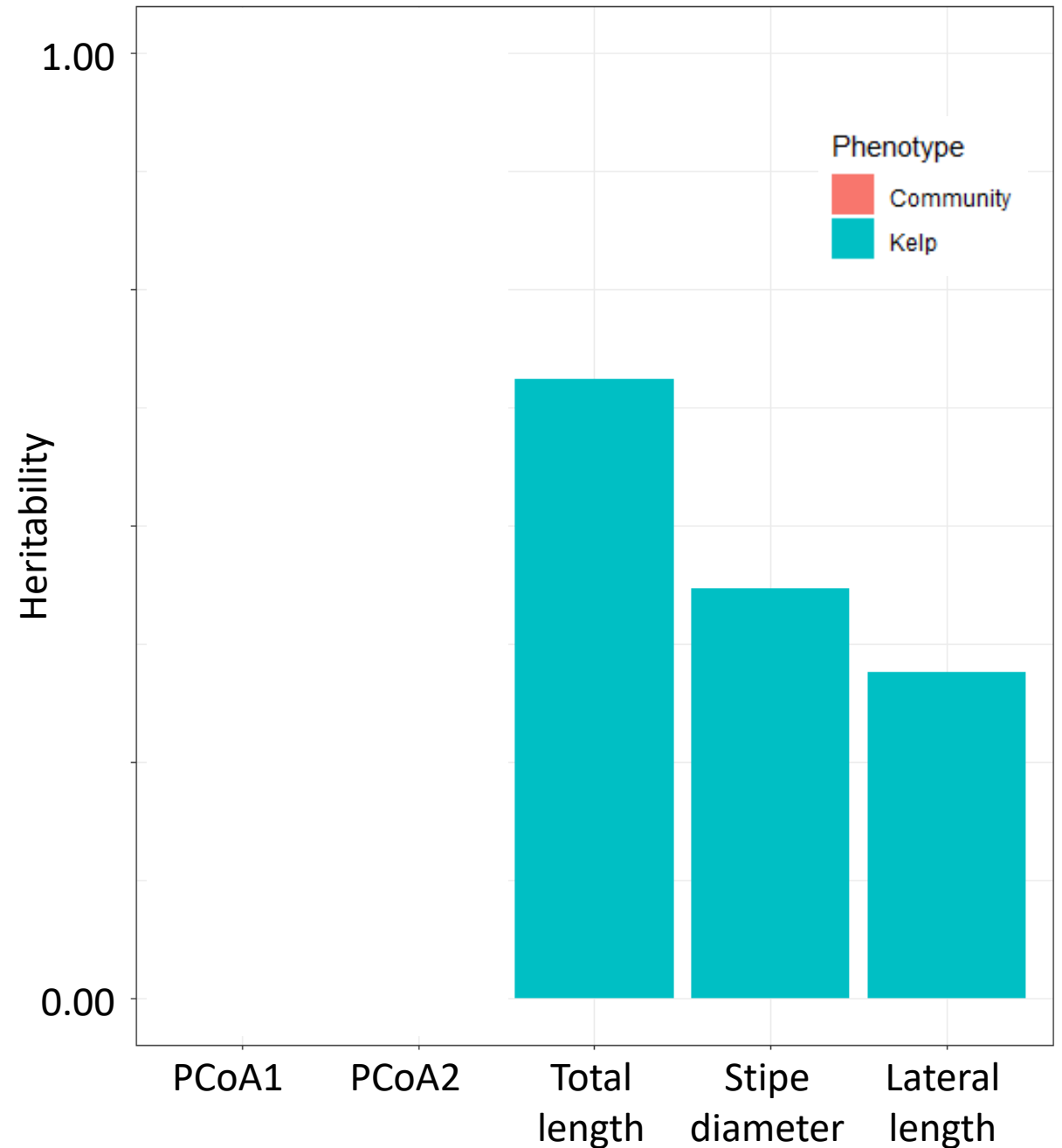
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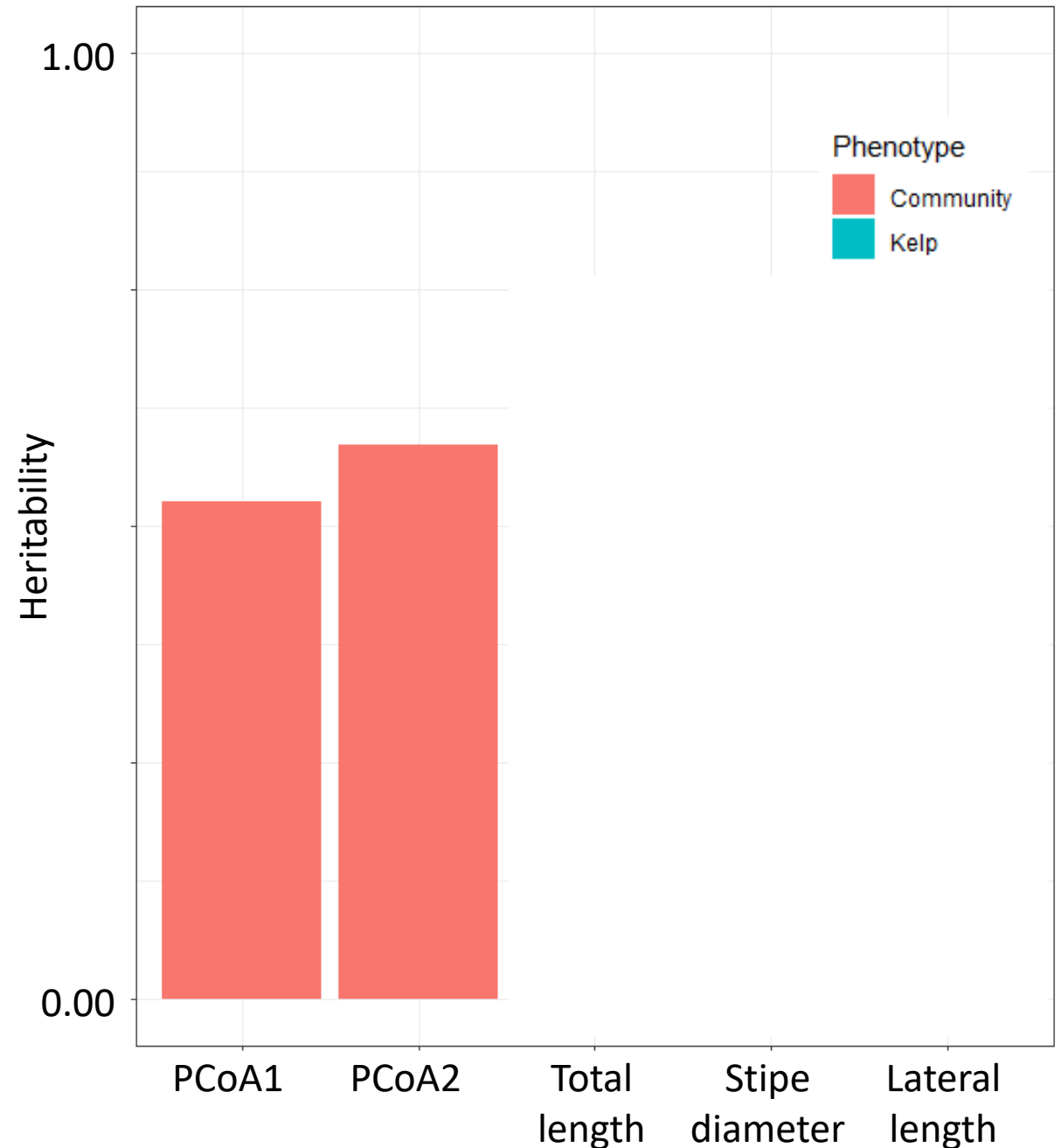
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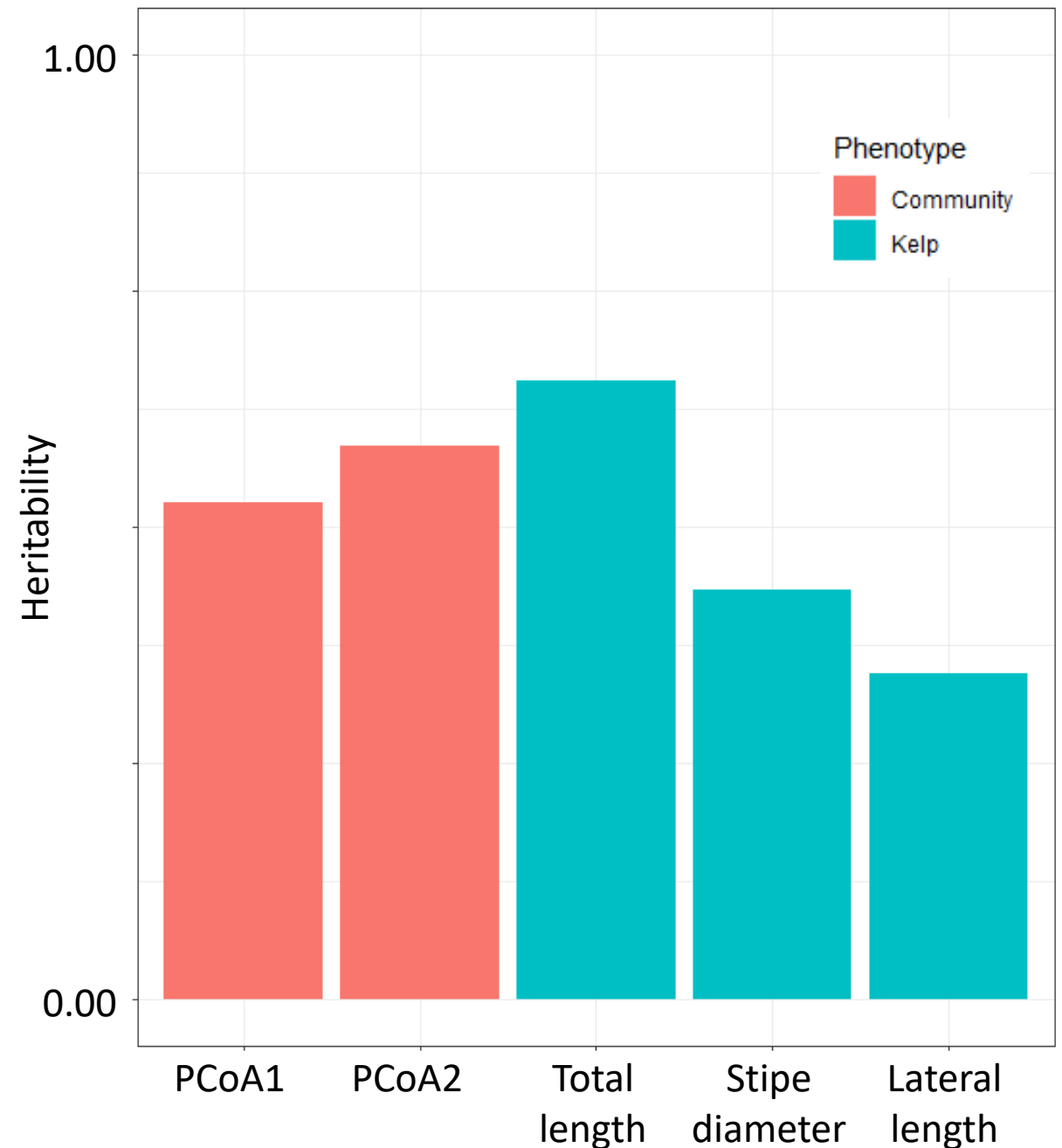
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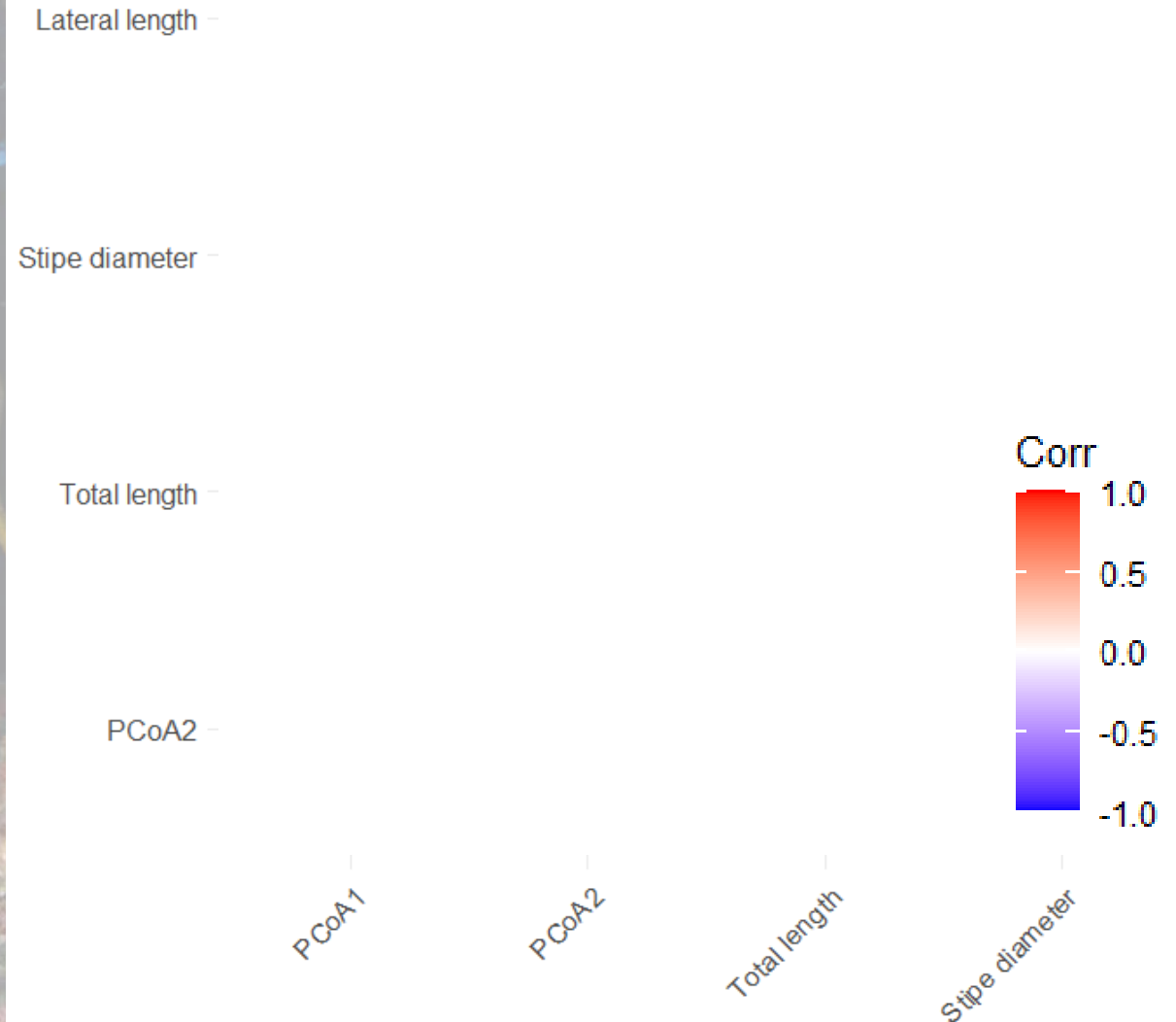
Direct and indirect genetic correlations

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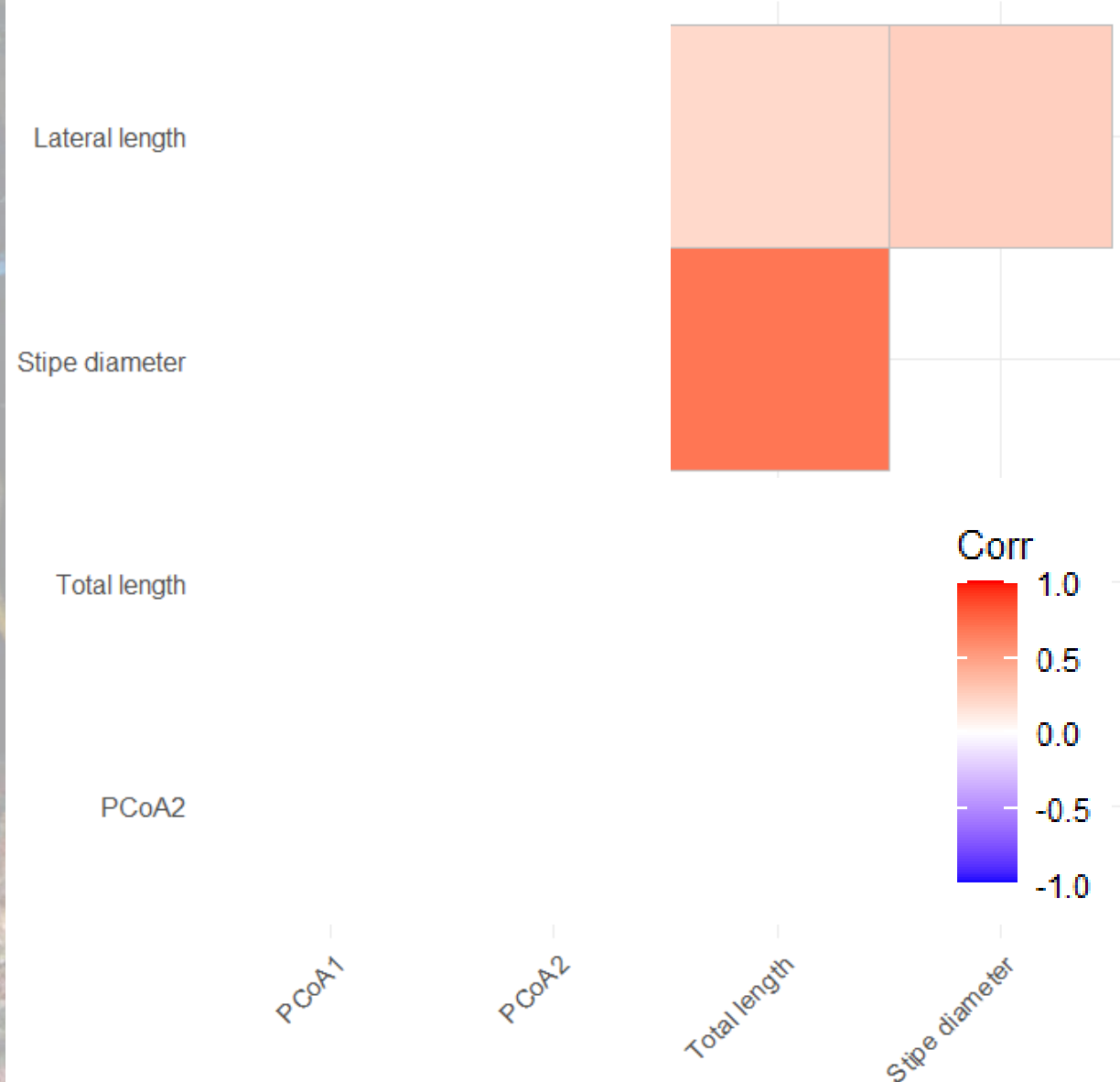
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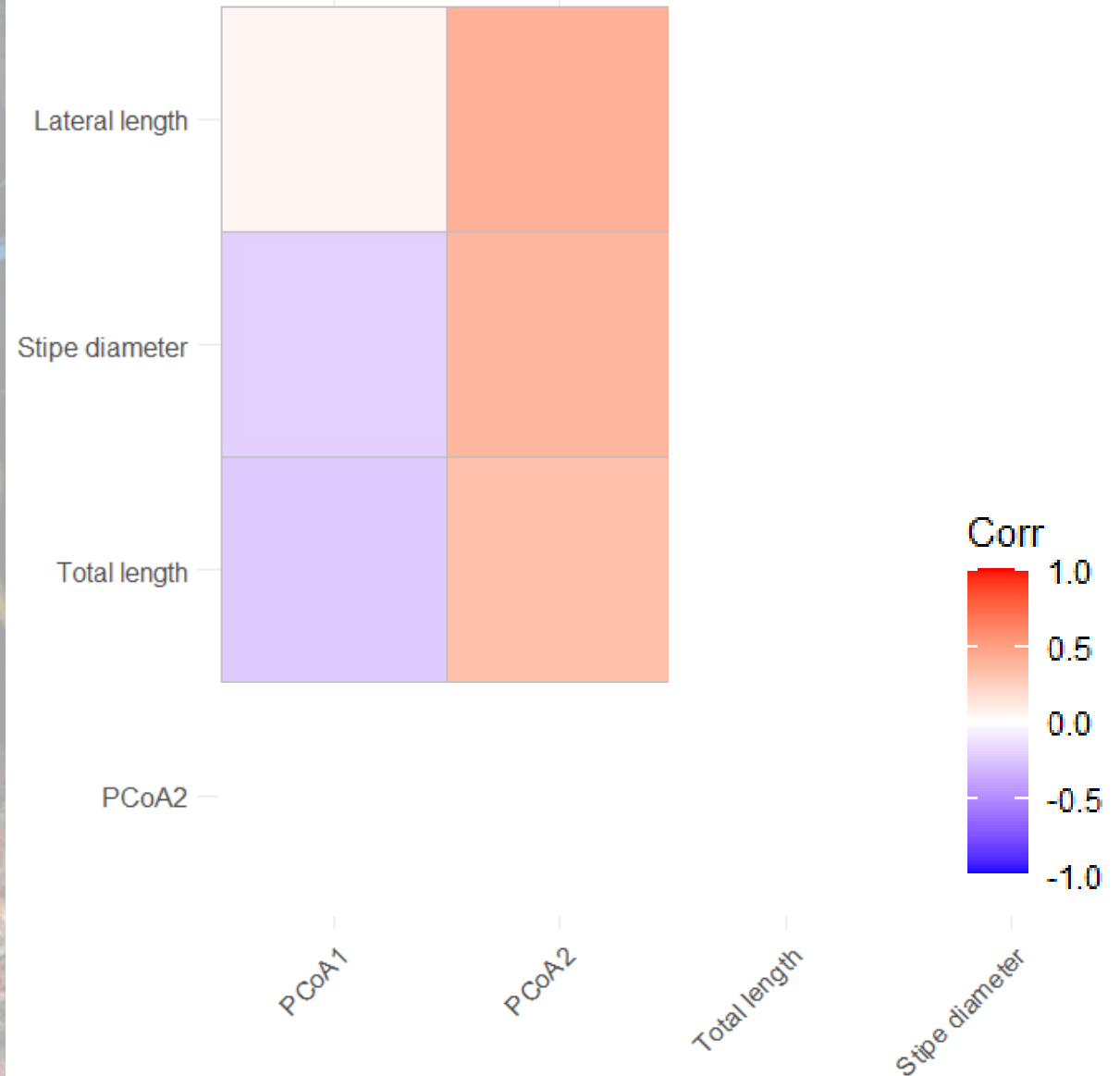
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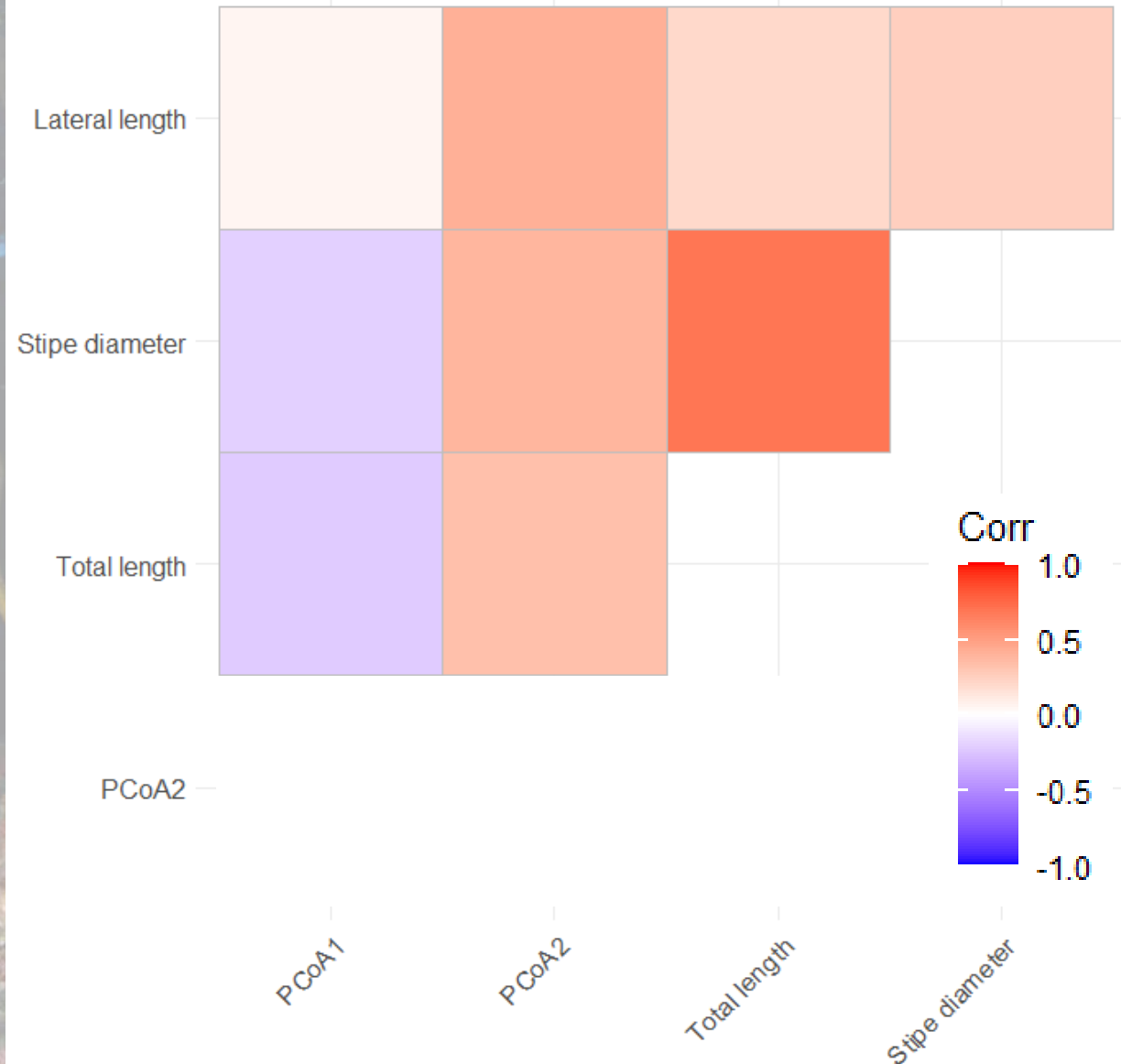
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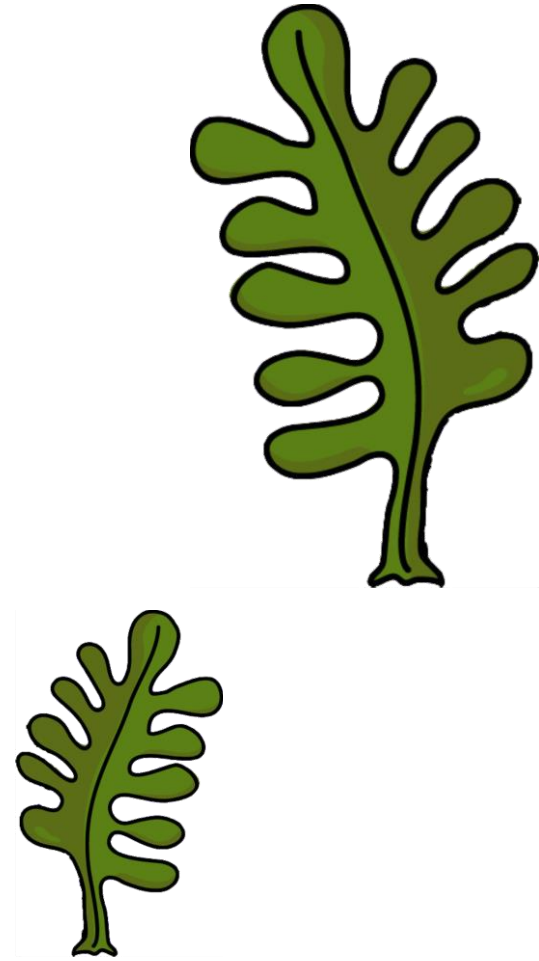
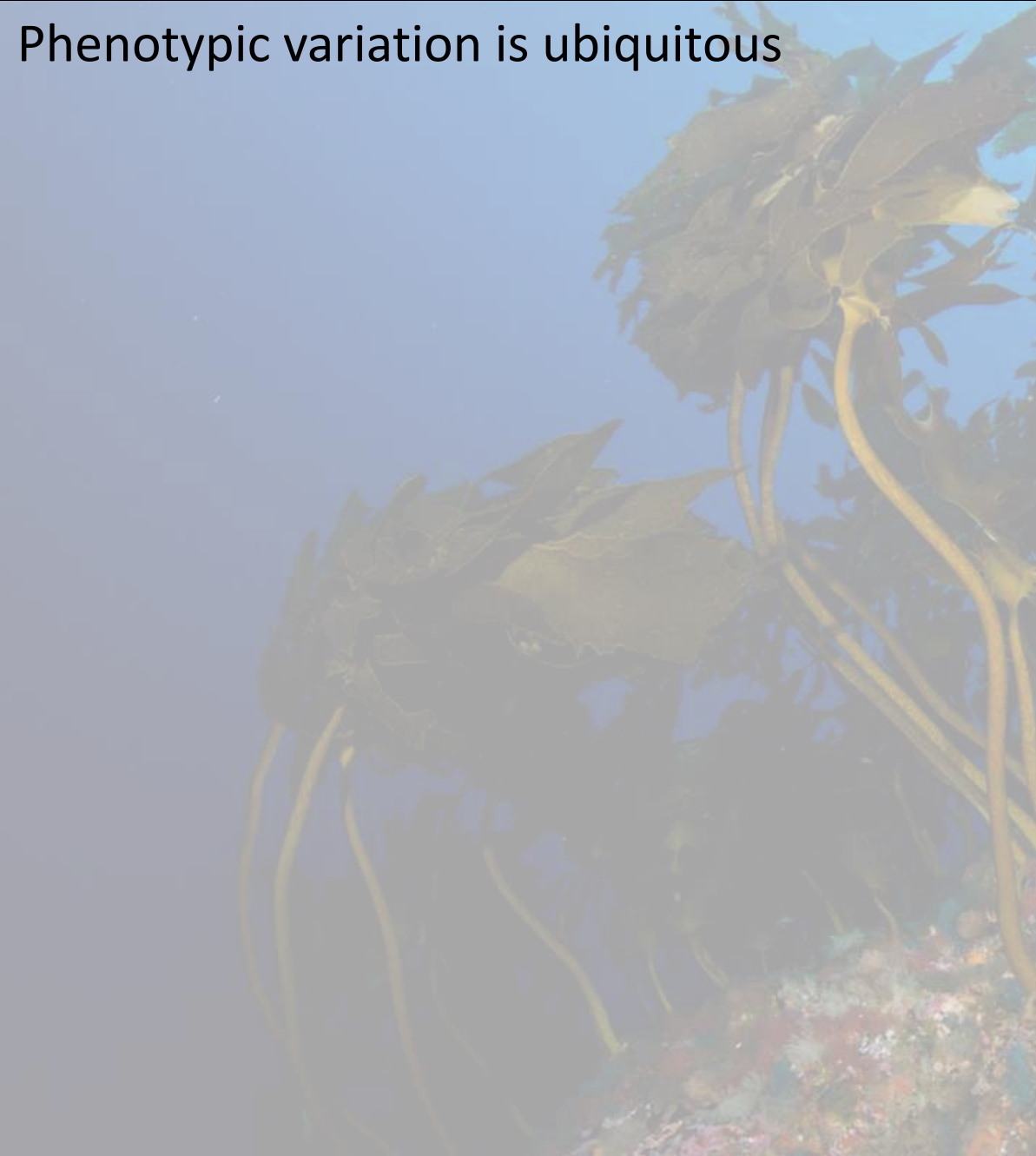
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Kelp forest eco-evolutionary dynamics

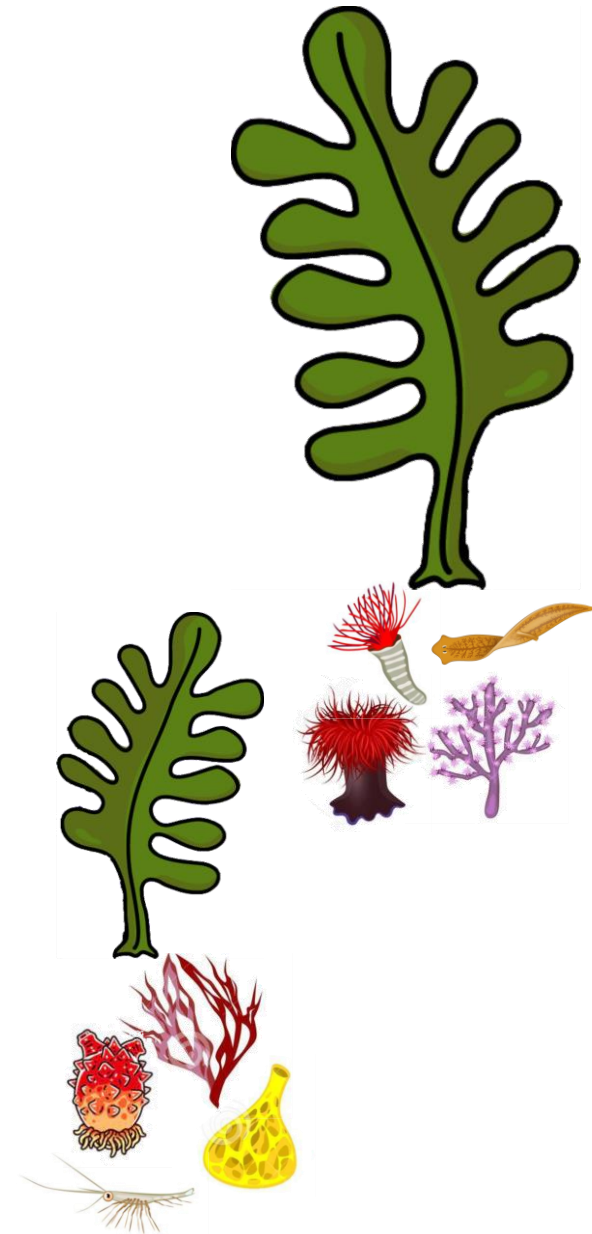
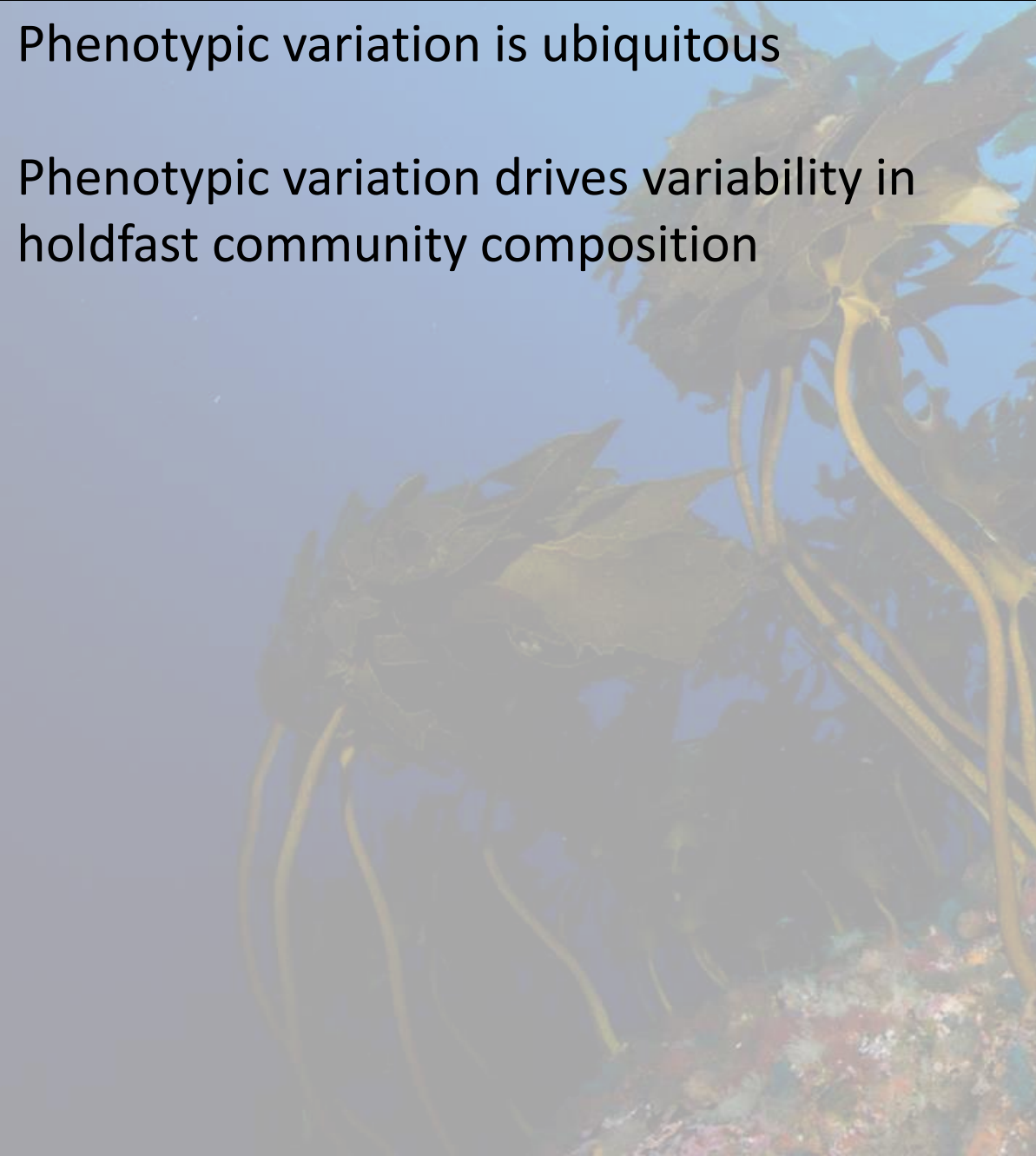
Phenotypic variation is ubiquitous



Kelp forest eco-evolutionary dynamics

Phenotypic variation is ubiquitous

Phenotypic variation drives variability in holdfast community composition

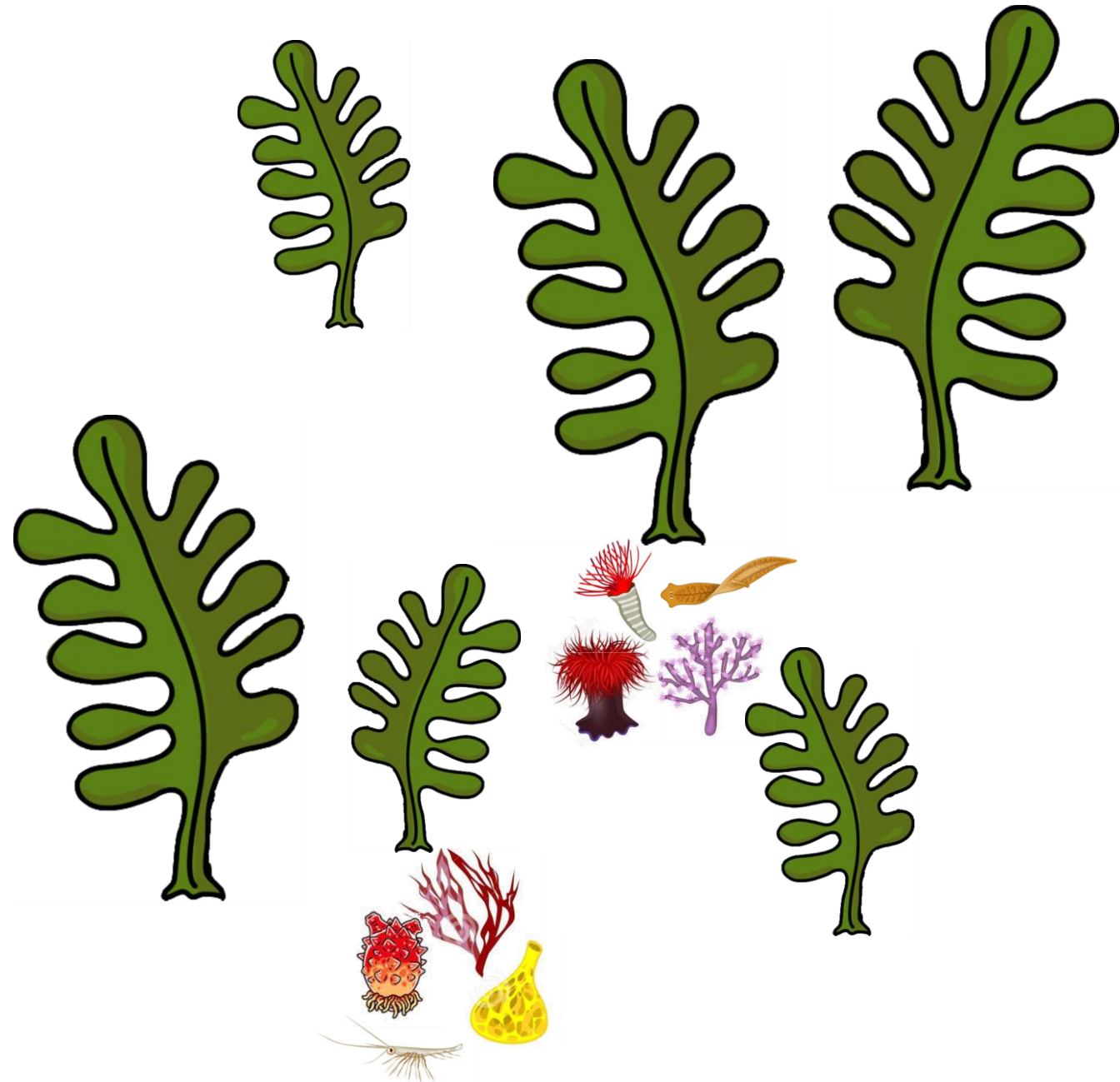
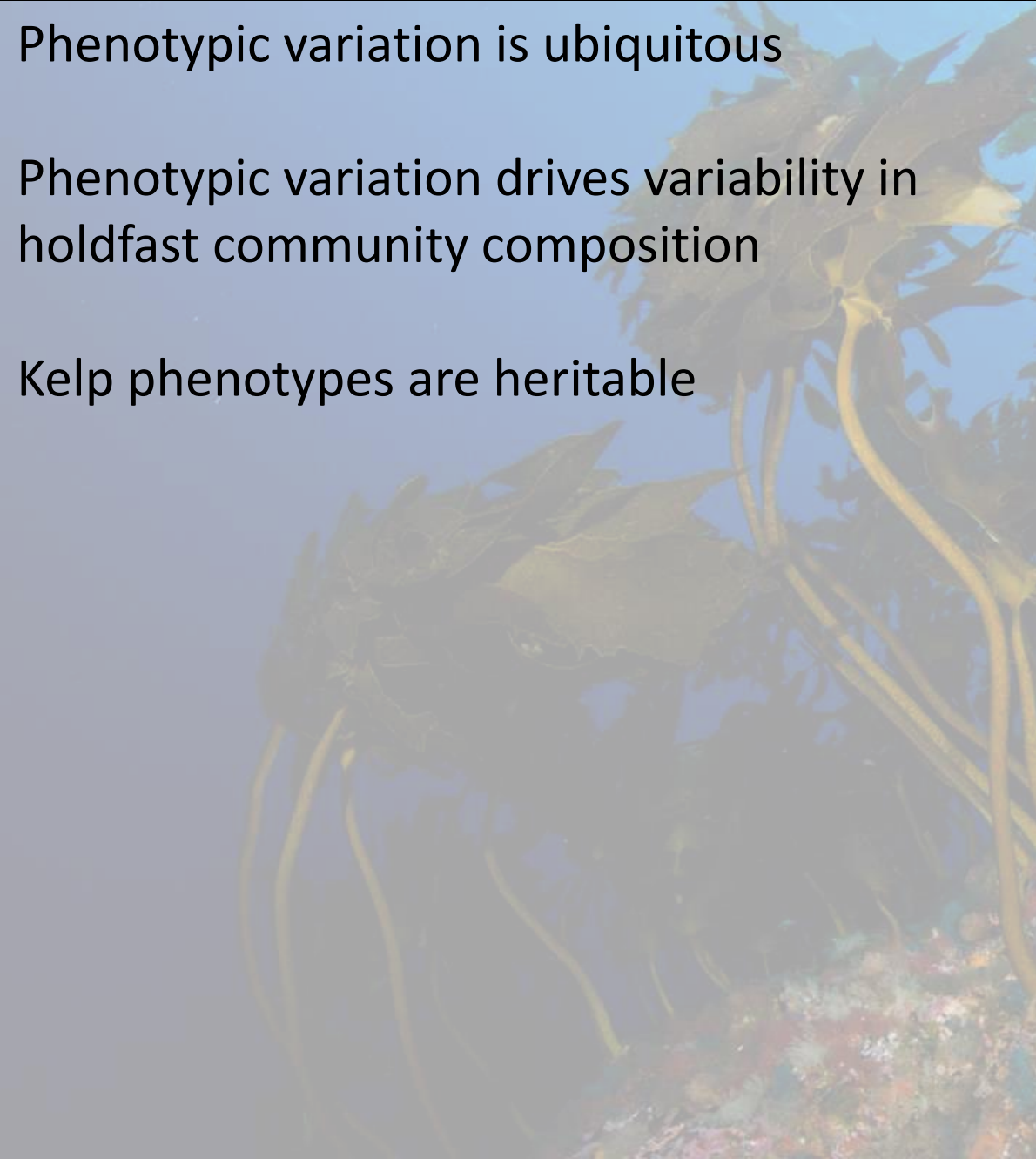


Kelp forest eco-evolutionary dynamics

Phenotypic variation is ubiquitous

Phenotypic variation drives variability in holdfast community composition

Kelp phenotypes are heritable



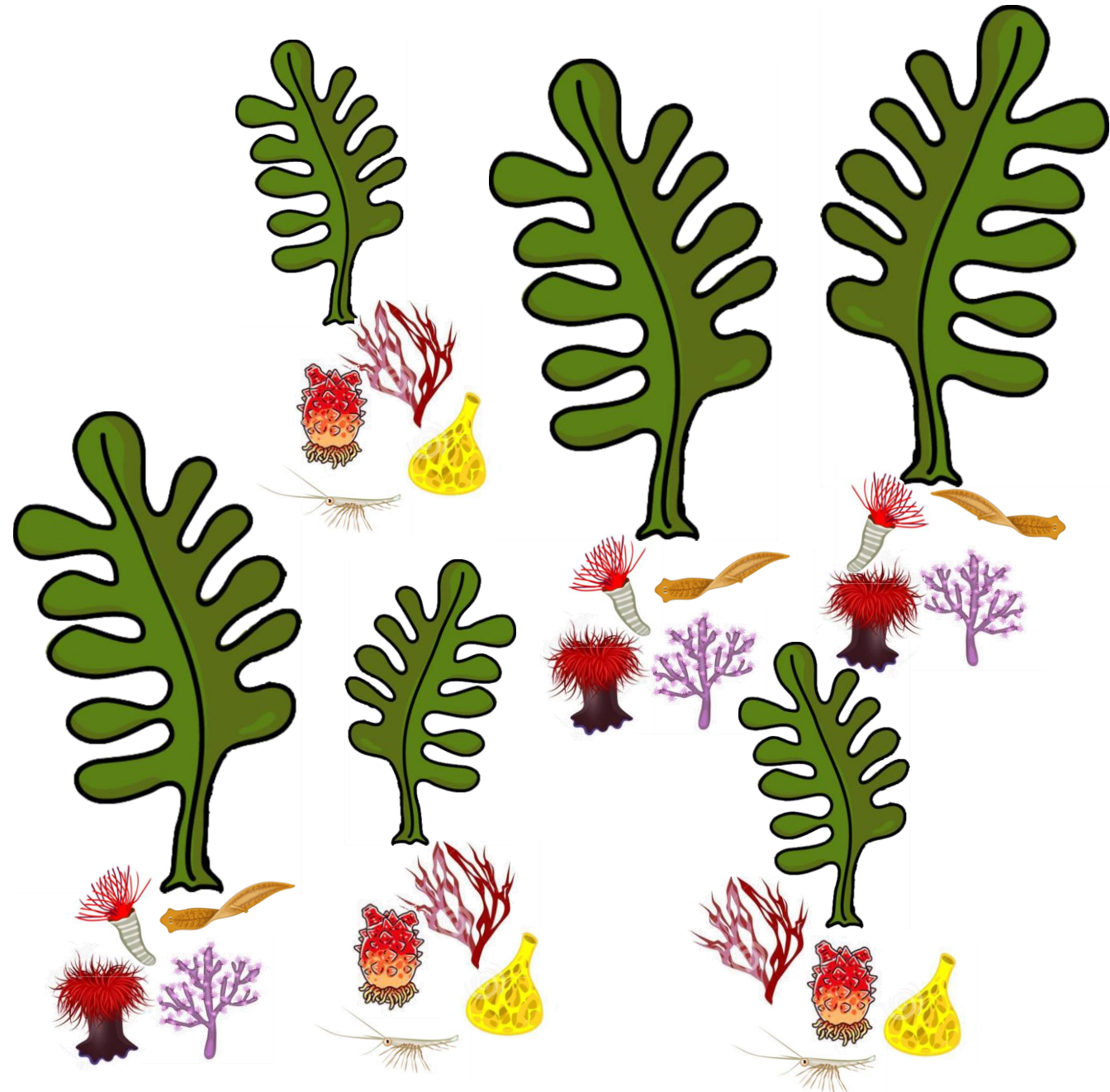
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Kelp phenotypes are heritable

Holdfast community composition is repeatable among kelp genetic lineages



Kelp forest eco-evolutionary dynamics

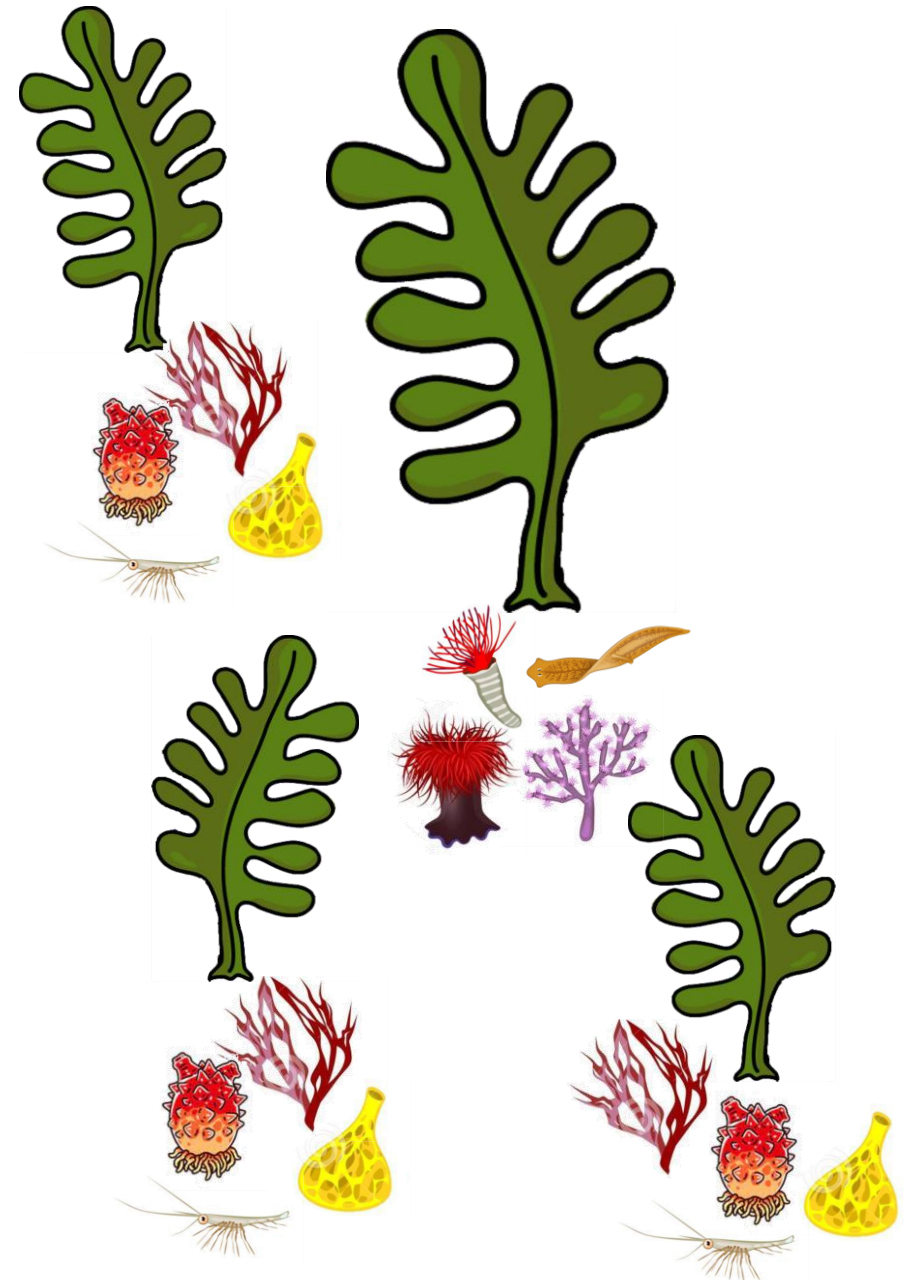
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Kelp phenotypes are heritable

Holdfast community composition is repeatable among kelp genetic lineages

Changes in the genetic composition of kelp populations will have an indirect effect on the distribution of biodiversity





Thanks!



MASSEY
UNIVERSITY

Collaborators: Marti Anderson, Wilma Blom, Todd Landers, Carol Diebel, William Pearman, Vanessa Arranz, Libby Liggins, Jose Ignacio Carvajal

Kelp army: Ella Lis, Beau Masters, Katie Littlewood, Carrie Reyden, Hochang Yoo, Jenny Ann Sweatman, Georgia Hrstich, Maddie Maclean, Emma Betty, Dave Wright, Irene Middleton & Emma Betty

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Docker: Edgar Valdez and Cristian Lopez

Marine metabarconding community: Owen Wangensteen, Xavier Turon, Ramon Gallego, Ulla Von Ammon, Amy van der Reis

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